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Applicant: WANG, et al

Title: PRIMERS, METHODS AND KITS FOR AMPLIFYING OR
DETECTING HUMAN LEUKOCYTE ANTIGEN ALLELES

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Sir:

Transmitted herewith for filing under 37 C.F.R. § 1.53(c) is the provisional patent application of:

Lu Wang
4425 N. Maryland Ave.
Shorewood, Wisconsin 53211
Citizenship: USA

Robert A. Luhm
N1699 15th Ave.
Wautoma, Wisconsin 54982-8305
Citizenship: USA

Enclosed are:

[X] Specification, Claims and Abstract (including figures) (106 pages).

The filing fee is calculated below:

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Please direct all correspondence to the undersigned attorney or agent at the address indicated below.

Respectfully submitted,

Date October 28, 2003

By 

FOLEY & LARDNER
Customer Number: 23524
Telephone: (608) 258-4991
Facsimile: (608) 258-4258

Robert N. Young
Attorney for Applicant
Registration No. 48,412

PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Lu Wang *et al.*

Title: **PRIMERS, METHODS AND KITS FOR AMPLIFYING OR DETECTING
HUMAN LEUKOCYTE ANTIGEN ALLELES**

Atty. Docket No.: 028979-0151

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P.O. Box 1450
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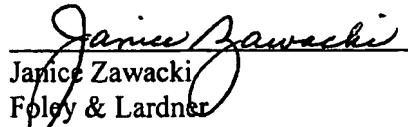
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Janice Zawacki
Foley & Lardner
P.O. Box 1497
Madison, Wisconsin 53701-1497
(608) 257-5035

Inventors: Lu Wang
Robert A. Luhm

U.S. PROVISIONAL PATENT APPLICATION

for

**PRIMERS, METHODS AND KITS FOR AMPLIFYING OR DETECTING HUMAN
LEUKOCYTE ANTIGEN ALLELES**

**PRIMERS, METHODS AND KITS FOR AMPLIFYING OR DETECTING
HUMAN LEUKOCYTE ANTIGEN ALLELES**

SUMMARY OF THE INVENTION

[0001] Embodiments of the present invention are set forth below:

[0002] A primer set comprising:
primers that are capable of amplifying all human leukocyte antigen (HLA) alleles of an HLA locus; and
a control primer pair that will produce an HLA control amplicon of predetermined size from the one or more HLA alleles if the one or more HLA alleles are present in the sample.

[0003] The primer set of the previous paragraph wherein the portion of the HLA allele amplified by the control primer pair is common to all or substantially all HLA alleles.

[0004] The primer set of paragraph [0002] or [0003] wherein the portion of the HLA allele amplified by the control primer pair comprises a portion of exon 4 of the HLA A locus or HLA B locus.

[0005] The primer set of any one of paragraphs [0002] to [0004] wherein the HLA control amplicon is about 500, 600, 700, 800, 900 or 1000 base pairs in length.

[0006] The primer set of any one of paragraphs [0002] to [0005] wherein the one or more HLA alleles are common to a single HLA locus.

[0007] A method for amplifying an HLA allele comprising:
performing a nucleic acid amplification reaction on a sample having or suspected of having one or more HLA alleles wherein the nucleic acid amplification reaction

comprises a primer set that is capable of amplifying one or more HLA alleles and a control primer pair that will produce an HLA control amplicon of predetermined size from the one or more HLA alleles if the one or more HLA alleles are present in the sample thereby providing an indication the presence or absence of HLA allele amplification.

[0008] The method of the previous paragraph wherein the portion of the HLA allele amplified by the control primer pair is common to all or substantially all HLA alleles.

[0009] The method of paragraphs [0007] or [0008] wherein the portion of the HLA allele amplified by the control primer pair comprises a portion of exon 4 of the HLA A locus or HLA B locus.

[0010] The method of any one of paragraphs [0007] to [0009] wherein the HLA control amplicon is about 500, 600, 700, 800, 900 or 1000 base pairs in length.

[0011] The method of any one of paragraphs [0007] to [00010] wherein the one or more HLA alleles are common to a single HLA locus.

[0012] A primer set comprising:
a mixture comprising a plurality of primers that are capable of simultaneously amplifying a plurality of a portion of class I HLA alleles simultaneously.

[0013] The primer set of the previous paragraph wherein the plurality of Class I HLA alleles belong to the same HLA locus.

[0014] The primer set of the previous paragraph wherein the HLA locus is HLA A or HLA B.

[0015] The primer set of the previous paragraph wherein the plurality of primers are capable of producing two amplicons spanning all alleles from the HLA locus.

[0016] The primer set of the previous paragraph wherein the first amplicon spans exon 1 to intron 3 and the second amplicon spans intron 3 to exon 5.

[0017] A method for amplifying a class I HLA allele comprising: performing a nucleic acid amplification reaction on a sample having or suspected of having a class I HLA allele wherein the nucleic acid amplification reaction comprises the primer set of any one of paragraphs [0012] to [0016].

[0018] The method of any one of paragraphs [0007] to [00011 or [0017]: sequencing any resulting HLA amplicons.

[0019] A primer for sequencing an HLA allele comprising: a forward primer comprising a 3' portion and a 5' portion wherein the 3' portion is complementary to an HLA allele of interest and the 5' portion is not complementary to the HLA allele of interest.

[0020] The primer of the previous paragraph wherein the 5' portion non-complementary portion is 1 to about 35 bases inclusive.

[0021] The primer of paragraphs [00019] or [0020] wherein the forward primer is for one of exons 2 and 3 in a B locus of the HLA allele.

[0022] The primer of any one of paragraphs [0019] to [0021] further comprising one or more additional primers that are complementary to one or more additional HLA alleles of interest.

[0023] A method for determining the sequence of an HLA allele comprising:

performing a sequencing reaction on an HLA allele using the primer of any one of paragraphs [0019] to [0022] 18-21; and determining the sequence of one or more HLA alleles.

BRIEF DESCRIPTION OF THE DRAWINGS

[0024] Figure 1 is a flowchart illustrating a specific procedure for sequencing an HLA allele according to a present method.

[0025] Figures 2A-2D are sequencing Electropherograms from the example.

DETAILED DESCRIPTION

[0026] Described herein are primer sets, methods and kits for amplifying and/or detecting human leukocyte antigen alleles. Some embodiments of the present invention provide primer sets and methods for amplifying HLA alleles.

[0027] On such primer set includes primers that are capable of amplifying all HLA alleles of an HLA allele subset or locus and also a control primer pair that is capable of producing an HLA amplicon of a defined size if the one or more HLA alleles are present in the sample. This primer set utilizes the target HLA allele as the template for the control primer pair and provides an indication the presence of absence of one or more HLA alleles. Any HLA alleles of the HLA allele subset or locus are also the template for the other primers in the primer set. As will be understood by the skilled artisan, in order to provide an effective control, the portion of the HLA allele amplified by the control primer pair is typically common to all or substantially all HLA alleles being tested for. In some embodiments, particularly when the target HLA locus is HLA A or HLA B, the portion of the HLA allele amplified by the control primer pair comprises a portion of exon 4. The primer set can be used in an amplification reaction to amplify an HLA allele and also provide a control. The control primer pair provides an indication of the efficiency of

any HLA allele amplification that occurs in the amplification reaction and also prevents false negative results. For example, if the results of the amplification provide an amplicon but lack the control amplicon, then the amplicon is likely a false negative. In contrast, if the control amplicon is also present then the amplification produced a positive result. In some embodiments, the primers of the control primer pair are selected such that any amplicon they produce will have a substantially constant size, such as 500, 600, 700, 800, 900 or 1000 base pairs, regardless of the HLA alleles that are present in the sample. As long as they do not interfere with the control parameters, the control primer pair can span a region with or without polymorphic positions. Accordingly, the portion of the HLA allele amplified by the control primer pair can have base polymorphisms but should lack any significant insertions or deletions.

[0028] Another primer set of the present invention contains a plurality of primer pairs, typically in the same solution, that are capable of simultaneously amplifying a plurality of class I HLA alleles simultaneously. As such, this primer set is capable of performing a successful multiplex amplification for all HLA alleles of an HLA allele subset or locus, such as the A locus, B locus or DR loci. In some embodiments, this multiplex amplification is achieved while still maintaining locus specificity because the product sizes produced from the amplification are considerably smaller.

[0029] Primer sets having combinations of the above characteristics can also be used. The above primer sets can be used to amplify any HLA alleles that are present in a sample.

[0030] The above primers and primer sets can be used in reaction that amplify HLA alleles. Suitable amplification reactions include those that proceed both linearly and exponentially. The present methods are also simplified as they can provide a common sequencing protocol for all HLA loci. Generally, the above

primer sets will contain primers that are sufficient to amplify all alleles of an HLA locus, such as HLA A, HLA B, etc. in a single reaction. Accordingly, the primers can be targeted to hybridize to non-specific regions of the chosen HLA locus so that all different HLA alleles can be successfully amplified. The primers can also be located so that the HLA amplicon resulting from the primers spans enough polymorphic positions of the locus so that individual alleles can be identified in a subsequent sequencing or typing reaction utilizing the HLA amplicon.

[0031] In some embodiments, where HLA A locus alleles are being amplified, the present primers can be selected to provide a single amplicon that includes exons 2, 3 and 4. Where HLA B locus alleles are being amplified, different primer sets can be used to produce dual amplicons that cover exons 2, 3 and 4. Some embodiments of the present primer sets, methods and kits utilize two separate amplifications in the B locus that reduces the number of potential heterozygotic combinations resulting in simplified sequence analysis, and the position of these split primers results in resolution of more of the locus thus reducing further the number of resultant ambiguities. For example, this can be achieved by amplifying the regions from exon 1 to intron 3 and intron 3 to exon 5 as two separate products simultaneously in one amplification mix. This results in a much more robust amplification. Amplifying these regions as two separate products is advantageous over a single product as this single product is frequently weak and hard to see on an agarose gel, particularly when modified nucleotides are required.

[0032] General and non-limiting position strategies for these primers is set forth in Table 1. In fact, the primer hybridization positions shown in this table can often be varied by one, two, five, ten, twenty or more positions, either upstream or downstream, and still provide acceptable results. Typically, when the primer hybridization position is moved upstream of the position illustrated in the table then additional bases can be added to the primer that hybridize further upstream which

can be accompanied by removal of bases from the opposite end of the primer. Similarly, when the hybridization position is moved downstream then bases are added to the primer that hybridize further downstream which can be accompanied by the removal of bases on the upstream hybridizing portion of the primer.

In HLA DR locus (Class II) amplification, one embodiment provides for a primer set that allows for eleven group specific amplifications that achieve resolution of DRB1, DRB3, 4 and 5 and exon 2.

[0033] The primers of the primer sets 3' terminus are capable of being extended by a nucleic acid polymerase under appropriate conditions and can be of any length, for example ranging from about 5 nucleotides to several hundred. Preferably, the primer oligonucleotide will have a length of greater than 10 nucleotides, and more preferably, a length of from about 12-50 nucleotides, such as 12-25 or 15-20. The primer oligonucleotides can also be chosen to have a desired melting temperature, such as about 40 to about 80°C, about 50 to about 70°C, about 55 to about 65°C, or about 60°C. The length of the primer is sufficient to permit the primer oligonucleotide to be capable of hybridizing to the target molecule. The sequence of the primer oligonucleotide is selected such that it is complementary to a predetermined sequence of the target molecule.

[0034] The present primer pairs can also be used individually to identify a single HLA allele, as desired. The present primers can be used in any method where nucleic acid primers find utility. For example, the primers are readily applicable to RT PCR of HLA mRNA for expression analysis because they target exon regions. The present primers can also be extended to, as yet, unknown HLA alleles.

[0035] One example of an assay where the present primer pairs find use include a detection assay or method for identifying an HLA allele in a sample

having, or suspected of having an HLA allele. In such an assay, generally, the sample will be contacted with the primer set under conditions such that the primer pair will amplify the HLA locus for which the primer pair is specific, if that locus is present in the sample. The presence or absence of the amplicon can then be determined or detected by standard techniques, such as separation techniques including electrophoresis, chromatography (including HPLC and denaturing-HPLC), or the like. Exemplary techniques for performing these assays are described in the examples section. As will be recognized by the skilled artisan the production of an amplicon will indicate the presence of an HLA locus in a sample. Accordingly, the presence or absence of an amplicon can be correlated with the presence or absence of the HLA locus in the sample. The sample to be detected can be obtained from any suitable source or technique.

[0036] Typically, nucleic acid amplification or extension involves mixing a target nucleic acid with a "master mix" containing the reaction components for performing the amplification reaction and subjecting this reaction mixture to temperature conditions that allow for the amplification of the target nucleic acid. The reaction components in the master mix can include a buffer which regulates the pH of the reaction mixture, one or more of the four deoxynucleotides (dATP, dCTP, dGTP, dTTP - preferably present in equal concentrations), that provide the energy and nucleosides necessary for the synthesis of DNA, primers or primer pairs that bind to the DNA template in order to facilitate the initiation of DNA synthesis and a DNA polymerase that adds the deoxynucleotides to the complementary DNA strand being synthesized. The polymerase used in the present methods and kits is not particularly limited, and any suitable polymerase can be used. Examples of suitable polymerase include thermostable polymerase enzymes, such as the TAQ polymerase Preferred polymerases have low error rates.

[0037] A typical thermal cycling reaction used in DNA amplification has a temperature profile of thermal cycling that involves an initial ramp up to a predetermined, target denaturation temperature high enough to separate the double-stranded target DNA into single strands. Generally, the target denaturation temperature of the thermal cycling reaction is approximately 91-97°C, such as 94°C- 96°C, and the reaction is held at this temperature for a time period ranging between 20 seconds to two minutes. Then, the temperature of the reaction mixture is lowered to a target annealing temperature which allows the primers to anneal or hybridize to the single strands of DNA. Annealing temperatures can vary greatly depending upon the primers and target DNA used. Generally, annealing temperatures range from 58°C - 70°C depending upon the application. Next, the temperature of the reaction mixture is raised to a target extension temperature to promote the synthesis of extension products. The extension temperature is generally held for approximately two minutes and occurs at a temperature range between the annealing and denaturing temperatures. This completes one cycle of the thermal cycling reaction. The next cycle then starts by raising the temperature of the reaction mixture to the denaturation temperature. Typically, the cycle is repeated 25 to 35 times to provide the desired quantity of DNA. As will be understood by the skilled artisan, the above description of the thermal cycling reaction is provided for illustration only, and accordingly, the temperatures, times and cycle number can vary depending upon the nature of the thermal cycling reaction and application.

[0038] Accordingly, the present primers, methods and kits can be used for research and clinical applications for any HLA associated disease, disorder, condition or phenomenon.

[0039] The present amplifications are preferably performed with a reaction volume and amount that is sufficient to perform a separation or detection step in

addition to providing enough amplified product in order to perform a sequencing reaction. Typically, amplification reactions having 25 μ l or more total volume are sufficient.

[0040] In some embodiments, a single multiplex amplification reaction can be run for all major HLA loci, e.g. HLA A, HLA B, HLA C, etc. in a single vessel. Generally, separate amplification reactions will be run for each HLA loci separately, and any of these separate reactions can employ a non-multiplex approach that produces amplicons that encompass all of the desired locus or a multiplex approach to produce amplicons that encompass shorter segments of the amplified locus. Such reactions can be run simultaneously or subsequently as desired.

[0041] Some of the present embodiments also provide complete locus resolution by employing locus specific primers located in the 5' and 3' untranslated areas of the gene. This can be approached in two distinct ways. The first can utilize an expansion and enhancement of the multiplex approach, where the entirety of the locus would be amplified from genomic DNA resulting in two or more products created simultaneously. This could be accomplished by two larger products, or potentially three smaller products. Secondarily, amplification of the locus using RNA as the starting template through simultaneous RT/PCR could provide total locus coverage with a manageable single product. This would provide ultimate resolution of HLA types.

[0042] After the HLA locus is amplified the specific alleles of the locus can then be determined by any method or assay known in the art. One such method is a sequencing reaction, for example the Sanger sequencing method. A description of such a general and specific sequencing method is set forth in Figures 1 and 1A. A detailed methodology is set forth in Appendix II. This sequencing reaction can be facilitated using a DYEnamic™ ET* Terminator Cycle Sequencing Kits available from Amersham Biosciences. Other suitable sequencing protocols include sequencing by

synthesis protocols, such as those described in U.S. Patent Nos. 4,863,849, 5,405,746, 6,210,891, and 6,258,568 and PCT applications WO 98/13523, WO 98/28440, WO 00/43540, WO 01/42496, WO 02/20836 and WO 02/20837.

[0043] Also provided is a primer set for sequencing HLA alleles and methods of sequencing HLA alleles which can use these primer sets. In some of these sequencing primers or detection methods, the 5' portion of one or more of the sequencing primers contains nonhomologous or sequence that does not hybridize to the HLA allele that can provide enhanced resolution of the sequence generated early in the polymerization reaction. Typically, the first bases resolved on any sequencing system are unclear. This tends to improve within 30 to 35 bases from the 5' end of the sequencing primer. By having or adding additional bases to the 5' end of the sequencing primer, the present primers with the non-complementary portion can achieve enhanced resolution of sequence. This design is particularly useful in sequencing primers that hybridize close to, for example within 10, 15, 20, 25, 30 or bases, of an intron/exon junction, for example where locus structure dictates placement of the primer close to the junction, such as occurs in exons 2 and 3. The number of the additional nonhybridizing bases on the 5' end of the specified sequencing primers can vary as desired, and for example can be one to 35 bases, such as two, three, four five, ten, fifteen, twenty, etc.

[0044] In some embodiments, HLA allele amplification can be joined together with an HLA sequencing reaction. Accordingly, the present primer sets, methods and kits can resolve greater than or about 50%, 55%, 60%, 65%, 70%, 75%, 80% or more of cis/trans ambiguities, including those found in the HLA B locus.

10X PCR Buffer

Tested from 0.5X- 2X concentration in the reaction, such as 1X.

MgCl₂

Class I reaction can typically range from 1.0mM – 2.0mM concentration in the reaction, for example 1.5mM.

Class II reaction from 1.5mM – 2.5mM concentration in the reaction, e.g., 2.0mM for one tube and 2.5mM for group specific amplification.

dNTP

0.5% - 2% concentration in the reaction, such as 1%.

[0045] For Class I , DMSO can be used at 5%-15% concentration in the reaction, for example 8%.

[0046] Primer concentration can vary and was successfully at ranges of 10 pmol/ μ l – 30 pmol/ μ l although optimal concentrations vary depending upon the reaction conditions, primer sequence and target sequence.

Product Specifications/QC Criteria

Background: Less than 20% of overall signal.

Evenness of het peaks: Must not be more than 30% difference. (I'm trying to get this changed to 50% difference)

Average signal strength:

Capillary = 100units – 4000 units. This is a very large range. But it was left that way to cover our bases. Typically, when signals get above 2000-2500 units, excessive background will result.

377 = 40 units – 4000units.. There is really no upper limit on this because the signals never get above about 500 units on the 377.

Coverage: The full sequence of the exon in question is readable from beginning to end.

[0047] Accordingly, preferred methods focus on identifying HLA alleles. The alleles of the HLA loci are classified as Class I – HLA-A, HLA-B, HLA-C, HLA-E, HLA-F and HLA-G, or Class II - HLA-DRA, HLA-DRB1, HLA-DRB2-9, HLA-DQA1, HLA-DQB1, HLA-DPA1, HLA-DPB1, HLA-DMA, HLA-DMB, HLA-DOA and HLA-DOB. There are over a hundred identified alleles that fall in some of these loci and these alleles are closely related and can differ in sequence by only one, or a few, positions. The HLA gene is discussed by Schreuder et al. in *Tissue Antigens*, 58:109 (2001) and the references disclosed therein, all of which are incorporated by reference. Additional information regarding HLA alleles, and in particular sequence information is available at www.ebi.ac.uk/imgt/hla and www.anthonynolan.org.uk/research.html.

[0048] Any or all of the present primers can be labeled with a detectable moiety, if desired, to facilitate detection. When present, the detectable moiety of the present invention is not particularly limited. Suitable examples of detectable labels include fluorescent molecules, beads, polymeric beads, fluorescent polymeric beads and molecular weight markers. Polymeric beads can be made of any suitable polymer including latex or polystyrene.

[0049] The present invention also provides arrays of the present primers that are contained within distinct, defined locations on a support. In some embodiments, the primers will be attached to the support in the defined location. The primers can also be contained within a well of the support. Each defined, distinct area of the array will typically have a plurality of the same primers. As used herein the term well is used solely for convenience and is not intended to be limiting. For example, a well can include any structure that serves to hold the nucleic acid primers in the defined, distinct area on the solid support. Non-limiting

example of wells include depressions, grooves, walled surroundings and the like. In some of the arrays, the primers at different location can have the same probing regions or consist of the same molecule. This embodiment is useful when testing whether nucleic acids from variety of sources contain the same target sequences. The arrays can also have primers with one or different primer regions at different location within the array. This embodiment can be useful where nucleic acids from a single source are assayed for a variety of target sequences. Combinations of these array configurations are also provided where some of the primers in the defined locations contain the same primer regions whereas other locations contain primers with primer regions that are specific for different targets. Any suitable support can be used for the present arrays, such as glass or plastic, either of which can be treated or untreated to help bind, or prevent adhesion of, the primer. In some embodiments, the support will be a multi-well plate so that the primers need not be bound to the support and can be free in solution. Such arrays can be used for automated or high volume assays for target nucleic acid sequences.

[0050] Although the present primers generally utilize the five standard nucleotides (A, C, G, T and U) in the nucleotide sequences, the identity of the nucleotides or nucleic acids used in the present invention are not so limited. Non-standard nucleotides and nucleotide analogs, such as peptide nucleic acids and locked nucleic acids can be used in the present invention, as desired. Several nucleotide analogs are known in the art (e.g., see, in Rawls, C & E News Jun. 2, 1997 page 35; in Brown, Molecular Biology LabFax, BIOS Scientific Publishers Limited; Information Press Ltd, Oxford, UK, 1991). In addition, the bases in a sequence may be joined by a linkage other than a phosphodiester bond, so long as the bond does not interfere with hybridization, such as in a peptide nucleic acid. These nucleotide analogs include any of the known base analogs of DNA and RNA such as, but not limited to, 4-acetylcytosine, 8-hydroxy-N6-methyladenosin-e, aziridinylcytosine, pseudoisocytosine, 5-(carboxyhydroxymethyl) uracil, 5-

fluorouracil, 5-bromouracil, 5-carboxymethylaminomethyl-2-thiou- racil, 5-carboxymethylaminomethyluracil, dihydrouracil, hypoxanthine, inosine, N6-isopentenyladenine, 1-methyladenine, 1-methylpseudouracil, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-methyladenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxy-aminomethyl-2-thiou- racil, beta-D-mannosylqueosine, 5'-methoxycarbonylmethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, oxybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, N-uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, orotic acid, 2,6-diaminopurine and the AEGIS™ bases isoC and isoG. As such, the primers can contain DNA, RNA, analogs thereof or mixtures (chimeras) of these components.

[0051] Universal nucleotides can also be used in the present primers. As used herein, universal nucleotide, base, nucleoside or the like, refers to a molecule that can bind to two or more, i.e., 3, 4, or all 5, naturally occurring bases in a relatively indiscriminate or non-preferential manner. In some embodiment, the universal base can bind to all of the naturally occurring bases in this manner, such as 2'-deoxyinosine (inosine). For example, the universal base can bind all of the naturally occurring bases with equal affinity, such as 3-nitropyrrole 2'-deoxynucleoside (3-nitropyrrole) and those disclosed in U.S. Patent Nos. 5,438,131 and 5,681,947. Generally, when the base is "universal" for only a subset of the natural bases, that subset will generally either be purines (adenine or guanine) or pyrimidines (cytosine, thymine or uracil). Examples of nucleotides that can be considered universal for purines are known as the "K" base (N6-methoxy-2,6-diaminopurine), as discussed in Bergstrom et al., Nucleic Acids Res. 25:1935 (1997) and pyrimidines are known as the "P" base (6H,8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one), as discussed in Bergstrom et al., supra,

and U.S. Patent No. 6,313,286. Other suitable universal nucleotides include 5-nitroindole (5-nitroindole 2'-deoxynucleoside), 4-nitroindole (4-nitroindole 2'-deoxynucleoside), 6-nitroindole (6-nitroindole 2'-deoxynucleoside) or 2'-deoxynebularine. A partial order of duplex stability has been found as follows: 5-nitroindole > 4-nitroindole > 6-nitroindole > 3-nitopyrrole. When used, such universal bases can be placed in polymorphic positions, for example those that are not required to specifically identify an allele. Combinations of these universal bases can also be used as desired. Primers and strategies using universal primers are discussed in U.S. Patent Application Serial No. 10/429,912.

[0052] The present invention also provides kits for carrying out the methods described herein. In one embodiment, the kit is made up of one or more of the described primer pairs with instructions for carrying out any of the methods described herein. The instructions can be provided in any intelligible form through a tangible medium, such as printed on paper, computer readable media, or the like. A plurality of each primer pair can be provided in a separate container for easy aliquoting. The present kits can also include one or more reagents, buffers, hybridization media, salts, nucleic acids, controls, nucleotides, labels, molecular weight markers, enzymes, solid supports, dyes, chromatography reagents and equipment and/or disposable lab equipment, such as multi-well plates (including 96 and 384 well plates), in order to readily facilitate implementation of the present methods. Such additional components can be packaged together or separately as desired. Solid supports can include beads and the like whereas molecular weight markers can include conjugatable markers, for example biotin and streptavidin or the like. Enzymes that can be included in the present kits include DNA polymerases and the like. Examples of preferred kit components can be found in the description above and in the following examples.

[0053] One embodiment of kit according to the present invention that can amplify and sequence HLA alleles is described below:

A Locus

Amplification Primers:

The 5' primer begins in the A Locus 5' untranslated region and ends in exon 1. The 3' primer is in exon 5. This is a locus specific amplification and all alleles are amplified with this primer set.

Sequencing Primers:

All sequencing primers are located in the introns flanking exons 2, 3 and 4.

B Locus

Amplification Primers:

Two 5' primers in exon 1. The alleles are divided roughly in half between the two primers as follows:

C Group		G Group		
070201	380201	1301	4002	5611
070202	390101	1302	4003	570101
0703	390103	1303	4004	5702
0704	390201	1304	4005	570301
0706	390202	1308	400601	5706
0709	3903	180101	400602	5801
0718	3904	1802	4008	5802
0801	3905	1803	4013	5804
0802	390601	1806	4020	5901
1401	390602	2702	44020101	7801
1402	3908	2703	44020102S	780201

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1405	3909	2704	440301	8101
15010101	3910	270502	440302	8202
1502	3917	270504	4404	8301
1503	3924	270505	4406	
1508	400101	2706	4407	
1509	400102	2708	4408	
1510	4007	2709	4409	
151101	4012	2711	4413	
151102	4016	2712	4431	
1512	4023	2713	47010101	
1513	4101	2714	47010102	
1514	4102	2718	4702	
1515	4201	350101	510101	
1516	4418	3502	510102	
151701	4501	3503	510105	
151702	4504	3504	510201	
1518	4601	3505	510202	
1519	4801	3506	5103	
1520	4802	3507	5104	
1521	4805	3508	5108	
1523	4901	3511	520101	
1525	5001	3512	520102	
1528	5002	3515	5204	
1529	670101	3528	5301	
1546	6702	3531	5401	
1552	7301	3541	5501	
1553		3542	5502	
1554		3543	5505	

1555	3701	5512
1557	3702	5601
1558	3704	5602
1566	3705	5603

There are four 3' primers in exon 5 (primers are multiplexed to cover the complexity of B Locus in this exon.)

Sequencing Primers:

All sequencing primers are located in the introns flanking exons 2, 3 and 4.

DRB1 One Tube

Amplification Primers:

[0054] There are 6 5' amplification primers which begin in intron 1 and end in exon 2. The primers are each designed to amplify a specific group of alleles: DRB1*01, DRB1*15/16/07, DRB1*03/11/13/14/8/12, DRB1*04, DRB1*09, and DRB1*10.

[0055] There is one 3' primer located in exon 2. All amplification primers are tailed with the M13 sequence. M13 sequence are tails added to the amplification primers, such as in DR and DQ, that allow the utilization of a single forward and reverse primer irrespective of groups. This results in a reduction in the total number of sequencing primers that must be included in the kit to cover all possible products. The tailing of the amplification primers was also done to assure full coverage of exon 2 upon sequencing.

Sequencing primers:

The sequencing primers are M13 forward and M13 reverse.

DRB1/3/4/5 Group Specific

Amplification primers:

[0056] The primers either begin in intron 1 and end in exon 2 or are fully in exon 2 depending on where the most specificity is for the group of alleles being

amplified. There are 11 5' Group specific primers amplifying the following groups/beta chains:

DRB1*01, DRB1*15/16, DRB1*03/11/13/14, DRB1*04, DRB1*07, DRB1*8/12, DRB1*09, DRB1*10, DRB3, DRB4, DRB5.

There is one 3' primer located in exon 2.

[0057] All amplification primers are tailed with the M13 sequence. The tailing of the amplification primers was done to assure full coverage of exon 2 upon sequencing.

[0058] Sequencing primers: The sequencing primers are M13 forward and M13 reverse.

[0059] Exemplary, but non-limiting, primer sets are described in the Tables and Appendices. Sequence alignments for assigning positions can be obtained by comparing the listed sequences with reported HLA sequences which can be found at www.ebi.ac.uk/imgt/hla and www.anthonynolan.org.uk/research.html. In the reported sequences, letter other than A, C, G or T indicate non-standard universal bases as follows: R, Y, S, M, W, and K are degenerate bases consisting of two possible bases at the same position. A or G = R, C or T = Y, G or C = S, C or A = M, A or T = W and G or T = K. There are also combinations of 3 possible bases at a particular base position known as H, B, V. Although primer pairs are often used in nucleic acid amplifications, the present primer sets can contain odd numbers of primers so that one or more forward primers can work in conjunction with a single reverse primer to produce an amplicon and vice versa. Appendix I provides a list of exon identities and ambiguous typing combinations of some HLA alleles that can be resolved by the present primer sets, methods and kits. Preferred kits include all reagents, primers, equipment etc. needed to perform the HLA amplification and/or sequencing except for the sample to be tested.

EXAMPLES

[0060] A and B Locus Multiplex Amplification

Genomic DNA was amplified with the following amplification mix:

A Locus

Reagent	Amount
Purified water	9.3ul
10X PCR Buffer	2.5ul
Magnesium Chloride	1.5ul
DMSO	2.0ul
dNTP (50% deazaG)	2.5ul
5'Primer- pA5-5	0.5ul
3'Primer- pA3-31	0.5ul
5'Primer- pA5-3	0.5ul
3'Primer- pA3-29-2	0.5ul
FastStart Taq	0.2ul
Genomic DNA	5.0ul
	25ul total reaction volume

B Locus

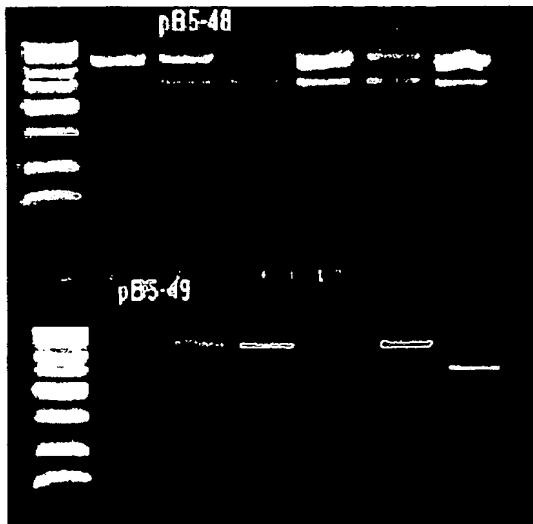
Reagent	Amount
Purified water	9.3ul
10X PCR Buffer	2.5ul
Magnesium Chloride	1.5ul
DMSO	2.0ul
dNTP (50% deazaG)	2.5ul
5'Primer- pB5-48 or 5-49	0.5ul
3'Primer- pB3-24	0.5ul
5'Primer- pB5-55 + 4	0.5ul
3'Primer- pA3-20,21,22,23	0.5ul
FastStart Taq	0.2ul
Genomic DNA	5.0ul
	25ul total reaction volume

The samples were run in a PE 9700 thermal cycler under the following conditions:

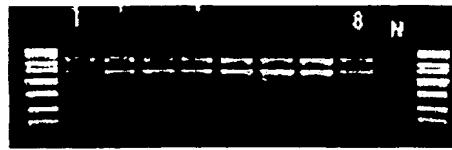
Initial Denaturation 95°C 4 min
Denaturation 95°C 20 sec
Annealing 63°C 20 sec 35 cycles
Extension 72°C 40 sec
Final Extension 72°C 5 min

The PCR amplicons were run on a 1.5% agarose gel

B Locus Agarose gel



A Locus Agarose gel



For A Locus, the 1200bp band is the product from pA5-3 and pA3-31 and the smaller 700bp band is the product from pA5-5 and pA3-29-2.

For B Locus, the 1200bp band is the product from pB5-48 or pB5-49 and pB3-24 and the smaller 700bp band is the product from pB5-55 + 4 and pB3-20,22,22 and 23.

4ul of ExoSAP-IT (USB) was added to each amplicon to rid each one of excess primer and dNTP. The amplicons were incubated at 37°C for 20 minutes and then at 80°C for 20 minutes.

Sequencing reactions for exons 2, 3 and 4 were prepared for each sample using the following mix of reagents:

DYEnamic ET Terminators	2ul
DYEnamic ET Terminator Dilution Buffer	2ul
Water	3ul
Sequencing Primer	1ul
ExoSAP-IT treated PCR product	2ul
	10ul total reaction volume

The sequencing reactions were cycled in a PE 9700 thermal cycler under the following conditions, with the first three steps being performed for 25 cycles:

95°C	20 sec
50°C	15 sec
60°C	60 sec
4°C	Infinite

Ethanol precipitation was used to remove excess terminators and precipitate out the sequencing products.

The precipitated products were run on an ABI 3100 capillary sequencer.

The Electropherograms are shown in figures 2A-2D.

[0061] The present primers and kits can have any or all of the components described herein. Likewise, the present methods can be carried out by performing any of the steps described herein, either alone or in various combinations. One skilled in the art will recognize that all embodiments of the present invention are capable of use with all other appropriate embodiments of the invention described herein. Additionally, one skilled in the art will realize that the present invention also encompasses variations of the present primers, configurations and methods that specifically exclude one or more of the components or steps described herein.

[0062] As will be understood by one skilled in the art, for any and all purposes, particularly in terms of providing a written description, all ranges disclosed herein also encompass any and all possible subranges and combinations of subranges thereof. Any listed range can be easily recognized as sufficiently describing and enabling the same range being broken down into at least equal halves, thirds, quarters, fifths, tenths, etc. As a non-limiting example, each range discussed herein can be readily broken down into a lower third, middle third and upper third, etc. As will also be understood by one skilled in the art all language such as "up to," "at least," "greater than," "less than," "more than" and the like include the number recited and refer to ranges which can be subsequently broken down into subranges as discussed above. In the same manner, all ratios disclosed herein also include all subratios falling within the broader ratio.

[0063] One skilled in the art will also readily recognize that where members are grouped together in a common manner, such as in a Markush group, the present invention encompasses not only the entire group listed as a whole, but each member of the group individually and all possible subgroups of the main

group. Accordingly, for all purposes, the present invention encompasses not only the main group, but also the main group absent one or more of the group members. The present invention also envisages the explicit exclusion of one or more of any of the group members in the invention.

[0064] All references, patents and publications disclosed herein are specifically incorporated by reference thereto. Unless otherwise specified, "a" or "an" means "one or more".

[0065] While preferred embodiments have been illustrated and described, it should be understood that changes and modifications can be made therein in accordance with ordinary skill in the art without departing from the invention in its broader aspects as described herein.

Claims

What is claimed is:

1. A primer set comprising:

primers that are capable of amplifying all human leukocyte antigen (HLA) alleles of an HLA locus; and
a control primer pair that will produce an HLA control amplicon of predetermined size from the one or more HLA alleles if the one or more HLA alleles are present in the sample, wherein the portion of the HLA allele amplified by the control primer pair is common to all or substantially all HLA alleles, wherein the portion of the HLA allele amplified by the control primer pair comprises a portion of exon 4 of the HLA A locus or HLA B locus, wherein the HLA control amplicon is about 500 base pairs in length and further wherein the one or more HLA alleles are common to a single HLA locus.

PRIMERS, METHODS AND KITS FOR AMPLIFYING OR DETECTING HUMAN LEUKOCYTE ANTIGEN ALLELES

ABSTRACT

[0066] The present invention describes primer pairs, methods and kits for amplifying, identifying and/or detecting HLA alleles.

FIGURE 1

PCR

Electrophoresis/ Agarose Gel

Hands on Time
1 hour

ExoSap-IT

Walk Away Time
7 hour

Sequencing Reactions

Gel Loading Preparation

Electrophoresis/Sequencer

Analysis

FIGURE 1A

DR Group Specific SBT

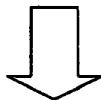
Amplification

Each of the 11 DR groups (DRB1*01, 15/16, 03, 04, 07, 8/12, 09,10, DRB3, DRB4, DRB5) is amplified with a given DNA sample.



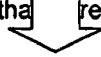
Agarose Gel

A separation, such as on an agarose gel, is performed and only those products that are positive will be taken further. (SSP).
*Minimum amount of products = 1 (e.g. DRB1*0101)
*Maximum amount of products = 4 (e.g. DRB1*0301,0701, DRB3*0101, DRB4*0101).



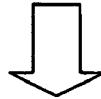
ExoSap-IT

All positive products have unused primers removed, such as with ExoSap-IT, and the product is diluted 1:1.5 with water due to the fact that there is so much product.



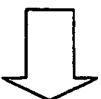
Sequencing Reactions

1 or 2 sequencing reactions (forward and reverse) are done for each positive product.

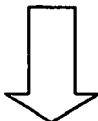


Excess Terminator Removal

Excess terminators are removed either by ethanol precipitation or by column purification.



**Products are resuspended and denatured for
gel/capillary loading.**



Samples are run on the sequencer.
The data collection program on the ABI (slab gel or capillary). Sample identification, voltage, run time, etc. are all controlled by this program.



Analysis
After the run is complete, the Sequencing Analysis program is opened and each sample is loaded into the sample manager and analyzed automatically by the software. Each product (forward and reverse) is analyzed and any bases that the software called incorrectly are corrected.



Allele Assignment
Once all electropherograms are corrected, they are put through typing software (MatchMaker, NCBI, etc) for allele assignment.

Table A Locus

				<u>Amount/rxn</u>	<u>Molarity</u>
pa5-3	HLA-A	AmpPrimer	CAGACSCCGAGGATGGCC	0.5uL	20uM
PA3-29	HLA-A	AmpPrimer	GCAGCGACCACGCCAG	0.5uL	20uM
PA5-5	HLA-A	5' Amp primer	ACC AGA AGT CGC TGT TCC CTY YTC AGG GA	0.5uL	20uM
pa3-31	HLA-A	3' Amp Primer	AAA GTC ACG GKC CCA AGG CTG CTG CCK GTG	0.5uL	20uM
pa3-29-2	HLA-A	Amp Primer	TCACRGAGCGACCAACAGCTCCAG	0.5uL	20uM
A 3' UT			GCCTTTGCAGAAACAAAGTCAGGGTTTC	0.5uL	20uM
Aex2F-2	HLA-A	seq primer	GCCTCTGYGGGAGAACAA	1uL	3uM
Aex2R-4	HLA-A	seq primer	GGATCTCGGACCCGGAGACTGT	1uL	3uM
Aex3F-2	HLA-A	seq primer	CCCGGGTTTCATTTCAGTTTAGG	1uL	3uM
Aex3R-3	HLA-A	seq primer	ATTCTAGTGTGGTCCCATTGTCTC	1uL	3uM
Aex4F	HLA-A	seq primer	GGTGTCCTGTCCATTCTC	1uL	3uM
Aex4R-4	HLA-A	seq primer	CAGAGGGCTCCTGGCTTC	1uL	3uM

A Locus Multiplex Amplification Primers

pa5-3	HLA-A	5' AmpPrimer	CAGACSCCGAGGATGGCC
PA5-5	HLA-A	5' Amp primer	ACC AGA AGT CGC TGT TCC CTY YTC AGG GA
pa3-31	HLA-A	3' Amp Primer	AAA GTC ACG GKC CCA AGG CTG CTG CCK GTG
pa3-29-2	HLA-A	3' Amp Primer	TCACRGAGCGACCAACAGCTCCAG

Table B Locus

					Location	Amount/rxn Molarity	
						0.5ul	20uM
pB3-24	HLA-B	3' Amp Primer	GGT KCC CAA GGC TGC TGC AGG GG		Intron 3, 1234-1256	0.5ul	20uM
pB5-48	HLA-B	Amp.	GAA CCG TCC TCC TGC TGC TCT C		Exon 1 base 20-41	0.5ul	20uM
pB5-49	HLA-B	Amp.	GAA CCG TCC TCC TGC TGC TCT G		Exon 1 base 20-41	0.5ul	20uM
					exon 5, 968-994	0.5ul	10uM each
					exon 5, 968-994	0.5ul	
					exon 5, 968-994	0.5ul	
					exon 5, 968-994	0.5ul	
pB3-20	HLA B rev	3' Amp Primer	ATC ACA GCA GCG ACC ACA GCT CCG AT				
pB3-21	HLA B rev	3' Amp Primer	ATC ACA GTC GCG ACC ACA GCT CCG AT				
pB3-22	HLA B rev	3' Amp Primer	ATC ACA GTC GCA ACC ACA GCT CCG AT				
pB3-23	HLA B rev	3' Amp Primer	ATC ACA GCA GCG ACC ACA GCG ACC AC				
pB5-55+4	HLA-B	5' Amp Primer	GGCTCTG ATT CCA GCA CTT CTG AGT CAC TTT AC		intron 3, 1308-1340	0.5ul	20uM
pB5-52	HLA-B	5' Amp primer	GAC CAC AGG CTG GGG CGC AGG ACC CGG		intron 1, 122-148	0.5ul	20uM
pB5-53	HLA-B	5' Amp primer	GAC CAC AGG CGG GGG CGC AGG ACC TGA		intron 1, 122-148	0.5ul	20uM
pB5-44	HLA B	5' Amp	ACGGCACCCCACCCCCGACTCAGAA		5' untranslated, -39 to -18	0.5ul	20uM
pB5-45	HLA B	5' Amp	ACGGCACCCCACCCCCGACTCAGAG		5' untranslated, -39 to -18	0.5ul	20uM
B 3' UT	HLA B	3' Amp	AGAGGCTCTTGAAAGTCACAAAGGGAA		3'untranslated,2913-2938	0.5ul	20uM
	yB2F-6a+10	HLA-B	SEQ Primer	ATTA TGA TTA AG CCC CTC CTC RCC CCC AG	Intron 1(~189-201)+nonsense bases	1ul	3uM
	yB2F-5a	HLA-B	SEQ Primer	CA GCC CCT CCT TGC CCC AG	Intron 1(~189-201)		
	yB2F-6a	HLA-B	SEQ Primer	AG CCC CTC RCC CCC AG	Intron 1(~189-201)		
	yB2F-7a	HLA-B	SEQ Primer	AG CTC CTC CTC GCC CCC AG	Intron 1(~189-201)		
	yB2F-12a	HLA-B	SEQ Primer	AG CCC CTC CTC GCC CCC AG	Intron 1(~189-201)		
	yB2R-4	HLA-B	Seq. Primer	GGA GGG GTC GTG ACC TGC G	Intron 1(~189-201)		
	yB3F-2a	HLA-B	seq.	GGG GAC GGG GCT GAC C			
	yB3F-2b	HLA-B	seq.	GGG GAC GGT GCT GAC C			
	yB3F-2c	HLA-B	seq.	AAACTCATGCCATTCTCCATTCA			
	B-Ex3R	HLA-B	SeqPrimer	GTCACATGGTGGTCCCTA			
	B-Ex4F1	HLA-B	SeqPrimer	GGCTCCTGCTTCCCTGAGAA			
	yB4R-3	HLA-B	Seq Primer				

Table C Locus

C Intron 3 R	GCAGTGGTCAAAGTGGTCA
C Intron 3 F	GCAGCTGTGGTCAGGCTGCT
C 3' UT	GGACACGGGGTGRGCTGTCTSTC
C5ApUTG	CAG TCC CGG TTC TGA AGT CCC CAG T
C5ApUTA	CAG TCC CGG TTC TAA AGT CCC CAG T
C5X1_I1GG	GGG CCG GTG AGT GCG GGG TT
C5X1_I1TA	GGG CCT GTG AGT GCG AGG TT
C5X1_I1TG	GGG CCT GTG AGT GCG GGG TT
C3ApX5A	AGC TCC AAG GAC AGC TAG GAC A
C3ApX5T	AGC TCC TAG GAC AGC TAG GAC A
C173ApX5	GAC AGC CAG GAC AGC CAG GAC A
C3ApI4T	GTG AGG GGC CCT GAC CTC CAA
C3ApI4C	GTG AGG GGC CCT GAC CCC CAA
C3ApI4TAC	GTG AGG GGC CCT TAC ACC CAA
CApExon5R2	GCC ATC ACA GCT CCT AGG ACA GCT A
CApExon5R3	GCC ACC ATA GCT CCT AGG ACA GCT A
CApExon5R4	GTG ACC ACA GCT CCA AGG ACA GCT A
CApExon5R5	AGC TAG GAC AGC CAG GAC AGC CA
CApExon5R1	CCA CCA CAG CTC CTA GGA CAG CTA
pC5-2	CAG TCC CGG TTC TRA AGT CCC CAG T
C5x21	GGA GCC GCG CAG GGA GG
c5x22	GGG TCG GGC GGG TCT CAG
c3x21	GGC CGT CCG TGG GGG ATG
c3x22	TCG KGA CCT GCG CCC CG
c5x31	TTC RGT TTA GGC CAA AAT CCC CGC
c5x32	GTC RCC TTT ACC CGG TTT CAT TTT C
c3x31	GCT GAT CCC ATT TTC CTC CCC TCC
c5x41	AGG CTG GCG TCT GGG TTC TGT G
c5x42	CCR TTC TCA GGA TRG TCA CAT GGG C
c5x43	CAA AGT GTC TGA ATT TTC TGA CTC TTC
c3x41	AGG ACT TCT GCT TTC YCT GAK AAG

Table DR Loci**DRB Group Specific Primers**

GSDR-01	5'-TGTAAAACGACGCCAGTCACG TTTCTTGTGGSAGCTT-3'
GSDR-15/16	5'-TGTAAAACGACGCCAGTTCC TGTGGCAGCCTAAGA-3'
GSDR-03/11/13/14	5'-TGTAAAACGACGCCAGTCGTT TCTTGGAGTACTCTACGTC-
GSDR-04	5'-TGTAAAACGACGCCAGTCGTT TCTTGGAGCAGGTTAAC-
GSDR-07	5'-TGTAAAACGACGCCAGTTCC TGTGGCAGGGTAAGTATA-
GSDR-08/12	5'-TGTAAAACGACGCCAGTCGTT TCTTGGAGTACTCTABGGG-
GRDR-09	5'-TGTAAAACGACGCCAGTGT TCTGAAGCAGGATAAGTT -
GSDR-10	5'-TGTAAAACGACGCCAGTCACA GCACGTTCTGGAGG-3'
GSDR-B3	5'-ACAGCTCCAGYGAWCACYAG-3'
GSDR-B4	5'-TGTAAAACGACGCCAGTAGCG AGTGTGGAACCTGATC-3'
GSDR-B5	5'-TGTAAAACGACGCCAGTGCAG CAGGATAAGTATGA-3'
GSDR-3' Universal	5'-CAGGAAACAGCTATGACCGCTY ACCTCGCCKCTGCAC-3'
CRP 1	5'-TCATGCTTTGCCAGACAG-3'
CRP 3	5'-GGCGGACTCCCAGCTTGTA-3'

DR Single Tube Amplification Primers

OTDR-01	TGTAAAACGACGCCAGTCCCACAGCACGTTCTTGTG
OTDR-02/07	TGTAAAACGACGCCAGTCCCACAGCACGTTCTGT
OTDR-03/5/6/08/12	TGTAAAACGACGCCAGTTCACAGCACGTTCTGGAGTAC
OTDR-04	TGTAAAACGACGCCAGTTACTAATCACGTTCTGGAGCAGG
OTDR-09	TGTAAAACGACGCCAGTTCCACAGCACGTTCTTGA
OTDR-10	TGTAAAACGACGCCAGTTACTAATCACGTTCTGGAGGAGG
OTDR-3-2	CAGGAAACAGCTATGACCCRYGCTYACCTCGCCKCTG

Sequencing Primers for both DR Methods (Group Specific and Single Tube)

M13 Forward	5'-TGTAAAACGACGCCAGT-3'
M13 Reverse	5'-CAGGAAACAGCTATGACC-3'

DR Single Tube Amplification Primers

OTDR-01	DRB1	5' Amp Primer	TGTAAAACGACGCCAGTCCCACAGCACGTTCTTGT
OTDR-	DRB1	5' Amp Primer	TGTAAAACGACGCCAGTCCCACAGCACGTTCTGT
OTDR-	DRB1	5' Amp Primer	TGTAAAACGACGCCAGTTCACAGCACGTTCTTGT
OTDR-04	DRB1	5' Amp Primer	TGTAAAACGACGCCAGTTACTAATCACGTTCTTGT
OTDR-09	DRB1	5' Amp Primer	TGTAAAACGACGCCAGTTCCACAGCACGTTCTTGT
OTDR-10	DRB1	5' Amp Primer	TGTAAAACGACGCCAGTTACTAATCACGTTCTTGT

FIGURE 2A

A Locus exon 2 forward

160 CAT CGC AG TGG GCT ACG TGG AC GAC ACG CAG 180
190 TTC GTG CGG TTG 200



FIGURE 2B

A Locus exon 2 reverse

40 TCG CAG TGG GCT A CGT GGA CGA CA CGC AGT TCG T GCG GTT CGA
350

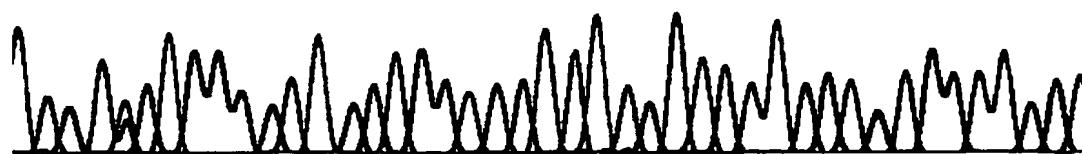


FIGURE 2C

B Locus Exon 2 Forward

190 ACC GGA AAC ACAC AGATCT UCAAG RCC H ASR CAC AG ACT G ACC G AG
200

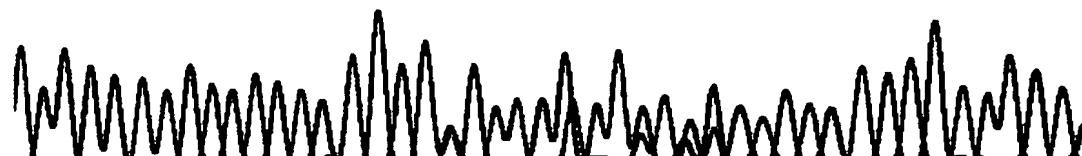


FIGURE 2D

B Locus Exon 2 Reverse

290 CCG GAA CAC ACAG ATCT UCAAG RCC H ASR CAC AG ACT G ACC G AG
300



SeCore™

POWERFUL HIGH RESOLUTION TYPING

DIRECT REVEAL

SeCore™ DESIGN CRITERIA

- Specific & Robust Chemistry
- High Resolution and Low Ambiguity
- Maximized Coverage of Alleles & Polymorphism
- Reliable Detection of Alleles and Polymorphism
- Flexible Throughput
- Ease of Use
- Compatible to Various Laboratory Instruments

DIRECT REVEAL

SeCore™ PCR

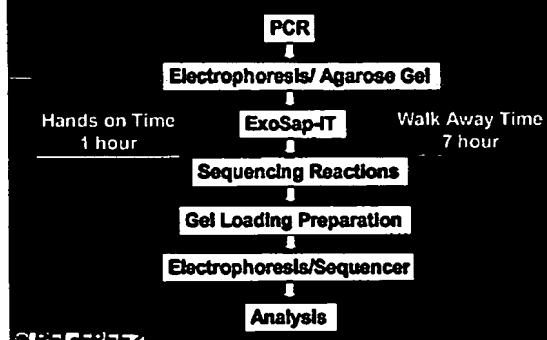
- Carefully Positioned Target Specific Primers
- Internal Control Eliminates False Negatives
- FastStart Taq DNA Polymerase
- Robust Buffer Condition – NO ALLELE DROP OUT

SeCore™ SEQUENCING

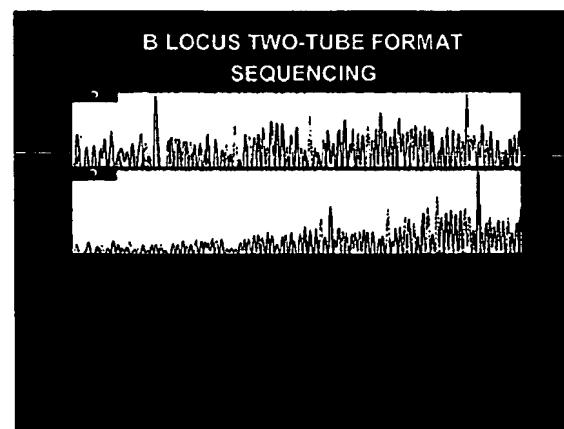
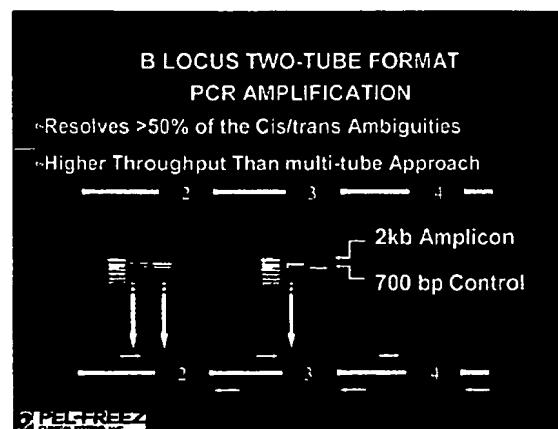
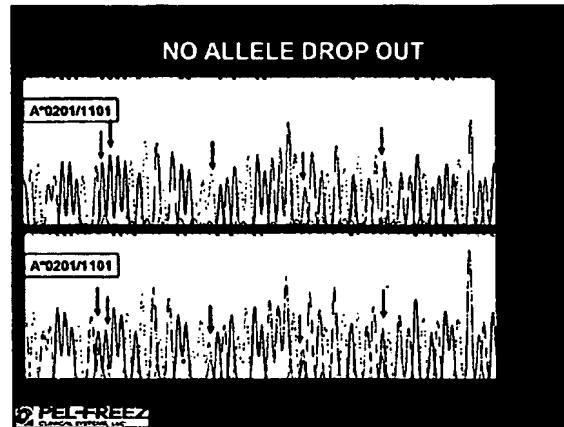
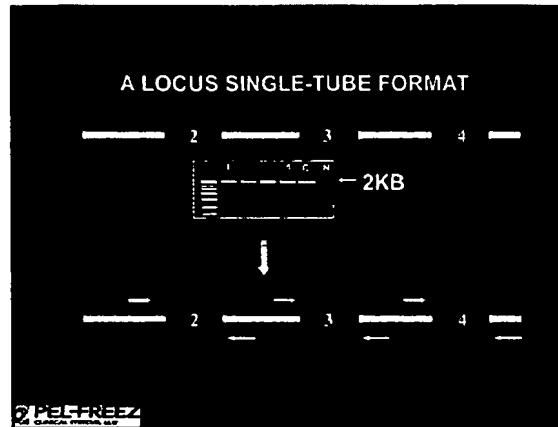
- Optimized DYEnamic™ ET Terminator Sequencing Chemistry
- Specific Sequencing Primers
- Appropriate Peak Intensity
- Robust Buffer Condition – NO ALLELE DROP OUT
- Clean Signals Generated in Proximity to Primer

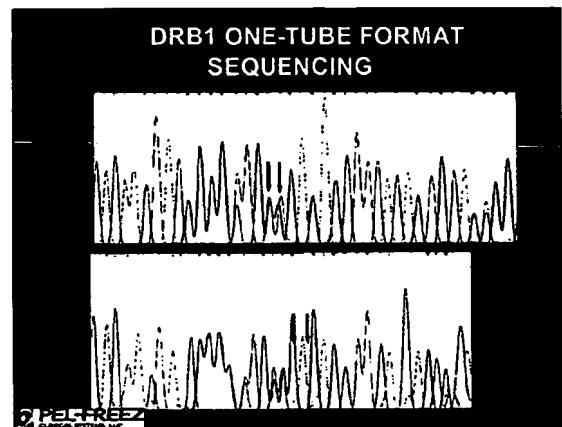
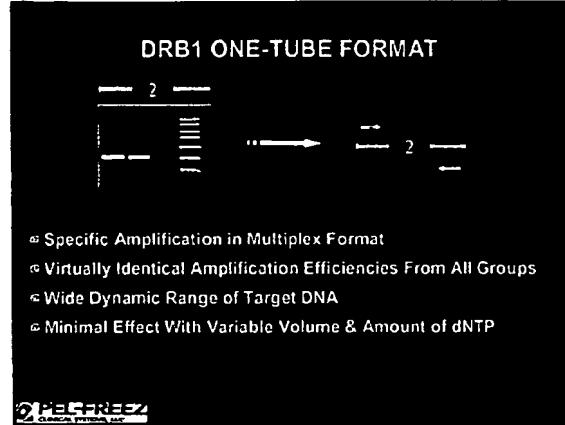
DIRECT REVEAL

SeCore™ PROCEDURE



DIRECT REVEAL

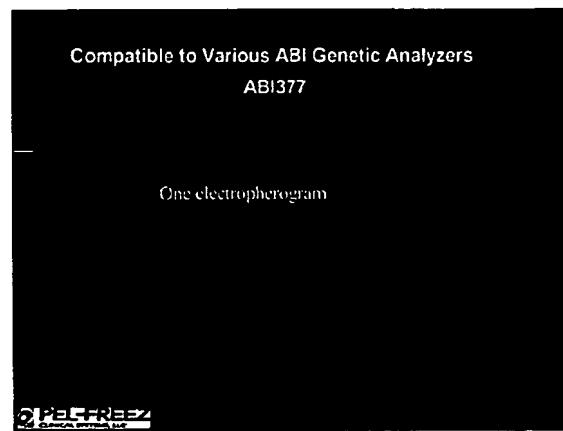
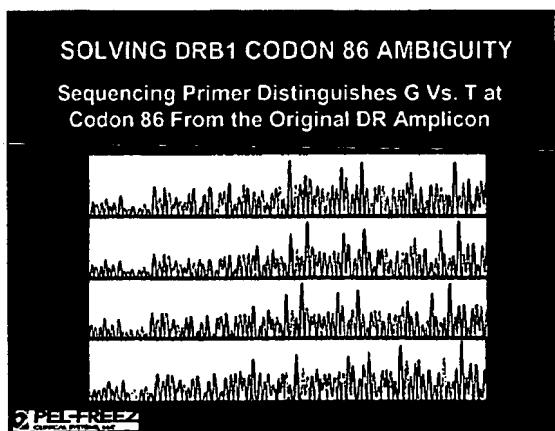
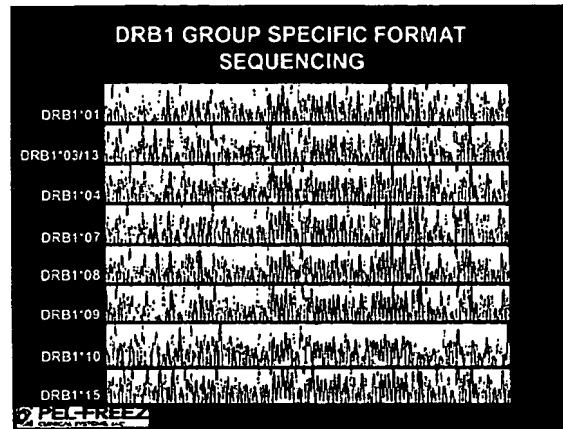
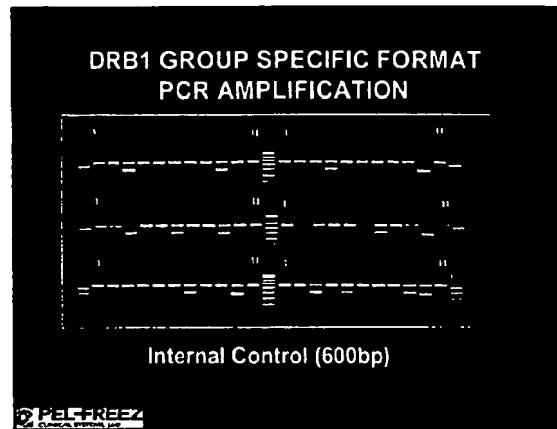




SeCore™ DRB1 GROUP SPECIFIC FORMAT

DRB1*01
DRB1*03/11/13/14
DRB1*04
DRB1*07
DRB1*08/12 ← 2 →
DRB1*15/16

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W W W W W W

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Class I

A Locus Single amplicon sequencing exon 2, 3 and 4 Resolves > 50% of *cis/trans* Antibodies
B Locus Dual amplicon sequencing exon 2, 3 and 4

Class II

DR Group Eleven group specific amplifications Amplification Internal Control
DRB1 Achieves the highest resolution of DRB1, DRB3, 4 and 5 exon 2
DRB1 Locus Single amplicon sequencing exon 2
Codon 86 Target specific GT sequencing mix to identify one of the two sample alleles from the original DR amplicon

Slab Gel Module

Membrane combs and their companion solutions provide an extremely simple method for sample loading the ABI 377XL.

The SeCore™ Line

Item Code	Product Name	Number of Tests
53000-25	SeCore™ A Locus Sequencing Kit	25
53100-25	SeCore™ B Locus Sequencing Kit	25
53200-25	SeCore™ Cw Locus Sequencing Kit	25
53300-25	SeCore™ DRB1 Locus Sequencing Kit	25
53310-25	SeCore™ DR Codon 86 Sequencing Kit	25
53396-25	SeCore™ DQB1 Sequencing Kit	25
53400-25	SeCore™ Slab Gel Sequencing Module	25
54000-1		1

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B Locus Dual amplicon sequencing exon 2, 3 and 4

Class II

DR Group Eleven group specific amplifications Amplification Internal Control
DRB1 Achieves the highest resolution of DRB1, DRB3, 4 and 5 exon 2
DRB1 Locus Single amplicon sequencing exon 2
Codon 86 Target specific GT sequencing mix to identify one of the two sample alleles from the original DR amplicon

Slab Gel Module

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Table 1

5' Untranslated Consensus Comparisons

A Locus	CARRAGCAGGGGTCAAGGGCCAGGGCCCCAGGGGTGGCTCTCAGRGTCAGGGGGTGTATGGATTG GGGAGTCCCAGCCTGGGATTCCCCAACTCC	GCAGTT
B Locus	GGRCGGGGCTCTCAGGGTCTCAGGCTCCAGGRCCCKYTYTGCAWTGGGAGGGCAGC	TGGGGATTCCCC
C Locus	RATCAGGACGAAGTCCC GGCGGGGYTCTCWGGGTCTCARCGTCCMAGGGCGTGTCTGCAYTGGGGAGGGCMGCGTTRAGGATTCYCC ACTCCCCCTGAGTT	
E Locus	CAAAGTGCTGAGATTACAGGGGTGAGCCACCGGCCAGCCAGGACTAATTCTAAAGAGTGTGCAGAGATAACCGAAACCTAAAA GTTTAAGAACCTGCT	GATTTGCTGGAAACTCTGGAGTT
F Locus	GGGGGTGTCTGGGTGGAGGCT CAGTATTGAGAATTCCCCATCTCCCCAGAGTT	GGGAGGGGGCAAAAGTCCCAGGGCCCCCAGGAGTGGCTCTCAAGGGCTCAGGGGG
G Locus	TGAGACAGAACGCTTGGCACAAAGAGTAGGGGGTCAAGGGCGAAGTCCAGGGCCTCAAGGGTGGCTCTCAGGGTCTCAAGGGCCC ACAGGGGTGTATGGRTGGGGAGGGCCCCGGTTGGGA	
H Locus	CAGGAGGAGGGGTCAAGGGCGAAGTCCAGGGCCCCAGGGGTGGCTCTCAGGGTCTCAGGGCCCGAAGGGGGTGTATGGATTG GGGAGGGCCCGCCTGGGATTGCCACCTCC	GCAGTT
J Locus	AGGAGGAGGGGTCAAGGGCGAAGTCCAGAGCCCCAGGGCATGGCTCTCAGGGTGTCTCAGGGGGCATGGCTG GGAGGTGCAGCATTGGGATTCCTCCATCTCCGAGGCC	
K Locus	AGGAGGAGGGGTCAAGGGCGAAGTCTATGGCCCCAGGGGTGGCTCTCAGGGTTTCAGGGCCGATGTATGATTG GGAGGCC AGGGTTGGGATTCCCCATCTCCGC	AGTT
L Locus	AGGAAAAGAGAGGGTCAAGGACAAGTCCCAGGGGG AGGCAGTGGCTCTGGGTCTCAGGGCCAAAGGGAGTGCACAGGGTGGGATTGCCACTCCCC TGAGTT	

A Locus CTTTCTCCCTCTSCCAACCTAYG
TAGGGTCTTCWTCCTGGATACTCACGAGCGGACCCAGTCTCACTCCCATTGGGTGTGGGTTCCAGAGAAGCCAATCAGTGTGGCGGGTGC
GTCKTCGGGGTGC

B Locus CACTTCTTCTC
CCACYTRTGBTCTGGGCTCTTCCAGGATACTSGTGACGCCRTCCCCAHTTCCCACTCCCATTGGGRTTYGGRTCTAGAGA
AGCCAATCAGYGYGTYGCCBGGTCC

C Locus CACTCTCTY CCAACCTGCGW
CGGTCTCTCTGAATACTCATGACGCCGTCGGCCAAATTCCCACACTCCCATTGGGTGTCGGRTT
CTAGAGAACCAATCAGGGTCTMCGCAAGTCC

E Locus TCCCCTTCCTCTGGATACTCATGACGCCAGACTCAGTTCTCATGGGTTCTAGAGAAG
AACCTGGTCATGGTCTCTGGATACTCATGACGCCAGACTCAGTTCTCATGGGAAATGGGTGTGGGTTCTAGAGAAG

C
F Locus CTCCTTCT CTC CCAACCCGTTGCAAG
TCCCTCTCCCTGGATACTCATACGCCCTCATTTCTCACTCCCATTGGGCTGSGTTCAGAGAACCAATCAGTGTGCGC

CGCAGTTC

G Locus TTCTCTCCTCCTGGATACTCACGCCCTCAGTTCTCACTCCCATTAGGTGACAGGGTTTAGAG
GGGCCTTCTGGATACTCACGCCCTCAGTTCTCACTCCCATTAGGTGACAGGGTTTAGAG

GTCTGG

H Locus CT CTTCTCTCACACCTG
CGACGGGTCCCTTTTCTGGATACTCAGGAAGGGCACAGTTCTCATGGGACTAGGTGTCGGGGTTCTAGAGAACCAATCAGTGTGCG
GTGGCGCCGGTCCC

J Locus CTTCTCTCCCTCAGGCCCTGGGACACTCACGAGGGACACTCACGAGGGACCCAGTTCTCACTCCCACACTGAG
TGTGGGGTTCTAGGGAAAGCCAATCAGGGTGGCG

K Locus CTCCTCTCCCTCTCCCAACTTATGTAGGGTGCCTTCTCCGGACACTCAGGATGTGGACTCAGTTCTCACCCCCATTGGTGTGC
GGGGTTCTAGGAAGCCAATGGGGTGGCTGGGTGCG
L Locus TGGTCTCCCAA
CCTCTCTGGATACTTCTCACTCCCATTCTCACCCCCATTGGGCTGGGGTTAGAGAACCAATCAGCTCGCC
GCGATCCC

PAS-3

A Locus	CKSTTCTAAAGYCCGCACGCACCCACGGGACTCAGATTCTCCCCAGACSSCGAGG
B Locus	CAGTTCTAAAGTCCCCACGGCACCCACCCGGACTCAGARTCTCCYCAGACRCCRAG
C Locus	C 5' UT
E Locus	CGGTTCTRAAGTCCCCAGTCACCCACCCGGACTCRSATTCTCCCCAGASGCCGAG
F Locus	TATAAAGTCCCCA TCCGGACTCAAG AAGTTCTC
G Locus	AGGACTCAGAGGTGGATC
H Locus	CCAGGTTCTAAAGTCCCACGCACCCGGGGACTCATATTTTCCC
J Locus	TTCTAAAGTCTCGCTCACCCACCCGGACT ATTCTCCCCAGACGCCAAGG
K Locus	GTTCTAAAGTCCCCACGGCACCCACCCGGGACTCGGAGTCTCCAGACGCCGAGC
L Locus	GGTTCTAAAGTCCCCACGGGAACCCATTGGGACTCAGATTCTCCCCAGACGCCGAG
M Locus	CTGTTCCAGAAGTCCCCAGAACCCATTGGGACTCAGATTCTCCCCAGACGCCAAGG
N Locus	AGACATAAGATCCCCGGCACTAC AGTCCCCGGCAACCACCCGGCACTCAGATTCTCCCCAAACGCCAAGG

PB5-44 and PB5-45

A Locus	ATG GCC RTC ATG SCK CCC CGA ACC CTC STC CTG CTA CTC TYG GGG GYY CTG GCC
CTG ACC CAG ACC WGG GCR G	PB5-48 and PB5-49
B Locus	ATG CKG GTC AYG GMG CCC CGA ACC STC CTC CTG CTC TSG GSR GCM STG GCC
CTG ACC GAG ACC TGG GCB G	
C Locus	ATG CGG GTC ATG GCG CCC CRA RCY CTC MYC CTG CTG CTC TCG GGA GSC CTG GCC
CTG AYC GAG ACC TGG RCC K	
E Locus	ATG GTA GAT GGA ACC CTC CTT TTA CTC YYC TCG GAG GCC CTG GCC
CTT ACC CAG ACC TGG GCG G	

Exon 1 Consensus Comparisons

A Locus	ATG GCC RTC ATG SCK CCC CGA ACC CTC STC CTG CTA CTC TYG GGG GYY CTG GCC
CTG ACC CAG ACC WGG GCR G	PB5-48 and PB5-49
B Locus	ATG CKG GTC AYG GMG CCC CGA ACC STC CTC CTG CTC TSG GSR GCM STG GCC
CTG ACC GAG ACC TGG GCB G	
C Locus	ATG CGG GTC ATG GCG CCC CRA RCY CTC MYC CTG CTG CTC TCG GGA GSC CTG GCC
CTG AYC GAG ACC TGG RCC K	
E Locus	ATG GTA GAT GGA ACC CTC CTT TTA CTC YYC TCG GAG GCC CTG GCC
CTT ACC CAG ACC TGG GCG G	

F Locus		ATG GCG CCC CGA AGC CTC CTC CTG CTG CTC TCA GGG GCC CTG GCC
CTG ACC	GAT ACT TGG GCG G	
G Locus	ATG GTG GTC ATG GCR CCC CGA ACC CTC TTC CTG CTR CTC TCG TGG GCC CTG ACC	
CTG ACC	GAG ACC TGG GCG G	
H Locus	ATG GTG CTC ATG GCG CCC CGA ACC CTC CTC CTG CTG CTC TCA GGG GCC CTG GCC	
CTG ACC	CAG ACC TGG GCG C	
J Locus	ATG GGG TC ATG GCG CCC CGA ACC CTC CTC CTG CTG CTC TCG TGG ACC CTG GCC	
CTG GCC	GAG ACC TGG GCG G	
K Locus	ATG GG GTC ATG GCG TCC CGA ACC CTC CTC CTG CTG CTC TTG GGG GCC CTG GCC	
CTG ACC	GAG ACC TGG GCG G	
L Locus	ATG GGG GTC ATG GCT CCC CGA ACC CTC CTC CTG CTG CTC TTG GGG GCC CTG GCC	
CTG ACC	GAG ACC TGG GCC G	

Intron 1 Consensus Comparisons

A Locus	GTG AGT GCG GGG TCG KG	AGG GAA ACS GCC TCT GYG GG	GAG AAG CAA SGG GCC
CKC CYG	GGG RCG CAR GAC CSG GGR	AG CCG CGC	

Aex2F-2

B Locus	GTG AGT GCG GGR TCG GS	AGG GAA ATG GCC TCT KYV GG	GAG GAG MRA GGG GAC
CGC AG	GGG GCK CAG GAC CYG RGG AG CCG CGC		
C Locus	GTG AGT GCG RGG TTR GG	AGG GAA DCG GCC TCT GSG GA	GAG GAR CGA GGG GCC
CKC CCG	GGC AGG GCG CAG GAC CCG GGG AG CCG CGC		
E Locus	GTG AGT GCG GGG TCG GG	ATG GAA ACG GCC TCT ACC GG	GAG TAG AGA GGG GCC
GGC CCG	GGG GCG AAG GAC TCG GGG AG CCG CGC		
F Locus	GTG AGT GCG GGG TCC AG AGA GAA ACG GCC TCT GTG GG	GAG GAG TGA GGG GCC	
CGC CCG	GTG GGG GCG CAG GAC TCA GGG AG CCG CSY		
G Locus	GTG AGT GCG GGG TCA GG	AGG GAA ACR GCC CCT CG	GAG GAG GGA GGG GCC
GGC CCG	GCG GGG GCG CAG GAC YCG GC	AG CCG CGC	
H Locus	GTG AGT GCA GGG TCT GC	AGG GAA ATG G	
CGC CCG	GGG GCG CAG GAC CCA GGG AG CCG CGC	TC	GG GAG GAG CGA GGG GCC

PB5-52 and PB5-53

C5x1_1GG/TG/TG		
-----------------------	--	--

J Locus	GTG AGT GCG GGG TCA GG	AGG GAA ACG GCC	TCT	GCC	GT	GAG	GAG CGA	AAG GTC
CAC CTG	GCT GGG GCG CAG GAC CCG	GGG AG CCG CGC						
K Locus	GTG AGT GCG GGA TCC GG	AGG GAA ATG GCC	TCT	GC	GGG	GAG	GAT	AGG GGC
CCG CGC	ACT GGG GCG CAG GAC CCG	GGG AG CAG CGC						
L Locus	GTG AGT GCG GGG TCG GG	AGG GAA AGG GCC	TCT	GC	GGG	GAG AAG	CGA GTG	GCC
CGC CCG		GC CCG GGG AG CCG CGC						

A Locus	CKG GAS GAG GGT CGG KYR GRT CTC ASC CAC TSC TCG YCC CCA G							
B Locus	CGG KAG GAG GGT CKG GCG GGT YTC AGC YCC TCC TDR CYC CCA G							
C Locus	AGG GAG GWG GGT CCG GCG GGT CTC AGC CMC TCC TCK YCC CCA G							
E Locus	CGG GAG GAG GGT CCG GAT CTC AGC CCC TCC TCG CCC CCA G							
F Locus	CCG GAG GAG GGT CTG GCG GGT CTC AGC CCC TCC TCG CCC CCA G							
G Locus	CGG GAG GAG GGT CCG GCG GGT CTC AAC CYC TCC TCG CCC CCA G							
H Locus	AGG GAG GAG GGT CCG GCG GGT CTC AGC TCC TCG CTC CCA G							
J Locus	CGG GAG GAG GGT CCG GCG GGT CTC AGC CCC TCC TCG CCC CCA G							
K Locus	AAG GAG GAG GGT CCG AGG GGT CTC AGC CCC TCC TCG CCC CCA G							
L Locus	CGG GAG GAG GGT CCG GCG GGT CTC AGC CTC TCC CCT CCA G							

YB2F-6a+10 YB2F-6-12

Exon 2 Consensus Comparisons

A Locus	GC TCY CAV TCC ATG AGS TRT WHC ACH TCC RTG TCC CSG CCC GGC MGY GRR							
RAG CCC	CGC TTC ATC KCM GTG GGC TAC GTG GAC RAC DCG							
B Locus	GC TCC CAC TYC ATG AGG YAT TTC BAC ACC KCY RTG TCC CGG CCY GKC CGC GGR							
GAG CYC	CSC TTC ATY DCM GTG GGC TAC GTG GAC GRC ACS							
C Locus	GC TCC CAY TCC ATG ARG TRT TTC KHC ACM KCY GTG TCC YGG CCY RGC SSC GGR							
GAG CCC	CRC TTC ATC KCA GTG GGC TAC STG GAC GAC ACR							
E Locus	GC TCC CAC TCC TTG AAG TAT TTC CAC ACT TCC GTG TCC CGG CCC GGC CGC GGG							
GAG CCC	CGC TTC ATC TCT GTG GGC TAC GTG GAC GAC ACC							

F Locus GC TCC CAC TCC TTG AGG TAT TTC AGC ACC GCT GTG TCG CGG CCC GGC CGC GGG
GAG CCC CGC TAC ATC GCC GTG GAG TAC GTA GAC GAC ACG
G Locus GC TCC CAC TCC ATG AGG TAT TTC AGC GCC GTG TCC CGG CCC GGC CGC GGG
GAG CCC CGC TTC ATC GCC ATG GGC TAC GTG GAC WCG
H Locus GC TCC CAC TCC ATG AGG TAT TTC TAC ACC ACC ATG TCC CGG CCC GGC CGC GGG
GAG CCC CGC TTC ATC TCC GTC GGC TAC GTG GAC GAT ACG
J Locus GC TCC CAC TCC ATG AGG TAT TTC AGC ACC GCC GTT TCC TGG CCG CGC CGC GGG
GAG CCC AGC TTC ATT GCC GTG GGC TAC GTG GAC GAC ACG
K Locus GT ACC CAC TCC ATA AGG TAT TTC AGC ACC GCC GTG TCC CGG CCG GGT CGC GGG
GAG CCC CGG TAC ATC GCA GTG GGC TAC GTG GAC GAC ACG
L Locus GC TCC CAC TCC TTG AGG TAT TTC AGC ACC GCA GTG TCC CAG CCC GGC CGC GGG
GAG CCC CGG TTC ATC GCC GTG GGC TAC GTG GAC GAC ACA

A Locus CAG TTM GTG CMG TTG GAC AGC GAC GSG AGC CRG ARG ATG GAG CYG YGG YGG GCR
CCG TRG ATR GAG CRG GAG RRK CCK GAG TAT TGG GAC SDG
B Locus CWG TTS GTG MGG TTC RAC AGC GAC GCC RCG AGT CMR AGR RNG GMK MCS CSG GCG
CCR TGG RTR GAG CAR GAG GGG CCD GNR YWT TGG GAS SVG
C Locus CAG TTC GTG CRG TTC GAC AGC GAC GCC GCG AGT CCR AGA GGG GAG CCG CGG CGG GMG
CSG TGG GTG GAG MAG GAG GGG CCG GAG TAT TGG GAC CGG
E Locus CAG TTC GTG CGC TTC GAC AAC GAC GCA GCG AGT CCG AGG ATG GTG CCG CGG CGC
CCG TGG ATG GAG CAG GAG GGG TCA GAG TAT TGG GAC CGG
F Locus CAA TTC CTG CGG TTC GAC AGC GAC GGC GCG ATT CCG AGG ATG GAG CCG CGG GAG
CCG TGG GTG GAG CAA GAG GGG CCC CAG TAT TGG GAG TGG
G Locus CAG TTC GTG CGG TTC GAC AGC GAC TCG GCG TGT CCG AGG ATG GAG CCG CGG CGC
CCG TGG GTG GAG CRG GAG GGG CCV GAG TAT TGG GAA GAG
H Locus CAG TTC GTG CGG TTC GAC AGC GAC GGC GCG AGG CAG ATG GAG CCG CGG CGC
CCG TGG ATG GAG CGG GAG GGG CCG GAG TAT TGG GAC CGG
J Locus CAG TTC GTG CGG GTC GAC AGT GAC GCC GTG AGT CTG AGG ATG AAG ACG CGG CGC
CGG TGG GTG GAG CAG GAG GGG CCG GAG TAT TGG GAC CTA
K Locus CAG TTC GTG CGG TTC GAC AGC GAC GCG ACT CCG AGG ATG TAG CCG CAG TCG
CCG TGG TTG GAG CAG GAG GGA CCG GAG TAT TGG GAC CGG
L Locus GAG TTC GTG CGG TTC GAC AGC GAC TCC GTG AGT CCG AGG ATG GAG CGG CGG CGC
CCG TGG GTG GAG CAG GAG GGG CTG GAG TAT TGG GAC CAG

A Locus	VAS ACA SGG MAW RTG ARG GSC CAS TCA CAG RBT VAY CGA GHG RRC CTG SRG AYC
SYG CDC	SGC TAS TAC AAC SAG AGC GAG GMC G
B Locus	RAS AYA CRG AHS WNS AAG VBC HMS RCR CRG RCT KRC MGA GWG RRC YTG CGS AHS
SYG CKC	SVC BAC TAC AAC CAG AGC KAG GMC G
C Locus	GAG ACA CAG AAS TAC AAG CGC CAG GCA CAG RCT GAC CGA GTG RRC CTG CGG AAM
CTR CGC	GCC TAC TAY AAC CAG AGC GAG GMC R
E Locus	GAG ACA CGG AGC GCC AGG GAC ACC GCA CAG ART TTC CGA GTG AAY CTG CGG ACG
CTG CGS	SGC TAC TAC AAT CAG AGC GAG GCC G
F Locus	ACC ACA GGG TAC GCC AAG GCC AAC GCA CAG ACT GAC CGA GTG GCC CTG AGG AAC
CTG CTC	CGC CGC TAC AAC CAG AGC GAG GCT G
G Locus	GAG ACA CGG AAC ACC AAG GCY CAC GCA CAG ACT GAC AGA ATG AAC CTG CAG ACC
CTG CGC	GGC TAC TAC AAC CAG AGC GAG GCC A
H Locus	AAC ACA CAG ATC TGC AAG GCC CAG GCA CAG ACT GAA CGA GAG AAC CTG CGG ATC
GCG CTC	CGC TAC AAC CAG AGC GAG GGC G
J Locus	CAG ACA CTG GGC GCC AAG GCC CAG GCA CAG ACT GAC CGA GTG AAC CTG CGG ACC
CTG CTC	CGC TAC AAC CAG AGC GAG GGC G
K Locus	AGC ACA CGG AAC ATC AGG CCC GCG CAC AGA CTG ACA AGA GTG AAC CTG CCC ATG
CCG CGC	CCG TAC TAC CAC CAG AGC TAG GCC G
L Locus	GAG ACA CGG AAC GCC AAG GGC CAC GCG CAG ATT TAC CGA GTG AAC CTG CGG ACC
CTG CTC	CGC TAT TAC AAC CAG AGC GAG GCC G

Intron 2 Consensus Comparisons

Aex2R-4	YB2R-4
A Locus	GTGAGTGACCCCRSCCSSGGGGCGCAGGTCAAGAC
ACGGACGGCCRGGTSRCCCA	CAGTCTCCGGTCCGAGATCCRCCCC
B Locus	GTGAGTGACCCCGGCCYGGGCCAGGTCAAGAC (CCC) CCCCAWCCCCS
ACGKACGGCCSGGGTCKCCYC	GAGTCTCYRGGTCCGAGATCCGGCCYGGAGG

CGCGGGRCYCCCG

CGCGGGGACCC G

C Locus GTGAGGTGACCCCRGGCCCCGGGCCAGGGTCMCAGACCCC TCCYCATTCCCC
 ACGGACGGCCGGGTGCCCCM RAGTCTCCSS TCTGAGATCCWCCCC RAGG (TGGAT) CTGGGAACCC G
 E Locus GTGAGGTGACCCCGGGCCAGGGGACAGGTCAAGGACACCCC TCCCCCATCCCC
 ACGGACGGCCGGTCCCTC GAATCTTGGTCCCAGATTCACCCCC AAG GCTGGGAACCC G
 F Locus GTGAGTGAMCCGGCCGGGGCAGGTCAAGGAC
 ACCCSOCCATTCGGYACGGGACCCGGGGTCCCYCM GAGTCTCCGGATCCGAAATCTACCCC GAGG
 CAGGGGA CCC G
 G Locus GTGAGTAACYCCGGCCAGGGMCAGATCACGACCCCCACCTCCATGCC
 ACGGACGSCCCCGGGTACTCTCC GAGTCTCCGGTCTGGATCCACCCC GAGG CCGGGGACCC G
 H Locus GTGAGTGACCCCCGGGGACGGCAGGTCAAGGACCC
 CCGGGTGCCTC GAGTCTCTGGTCTCGAGATCCTCCCC GAAA CCGGGGACCC
 J Locus GTGAGTGACCCCCGGGGCGAGATCACTTACTCCCCGCTCCATGCC
 GAGTCTCCGGTCAAGATCGACCCC GAGG CTGGGGACCT G
 K Locus GTGAATGACCCCCGGCTGGGGCAAGGTCACGACCC
 ACGGACGGCCGGTCCCCCGGAGTCTCCGGCTCAAGATCCACCCC GAGG CTGGGGACCC G
 L Locus GTGAGTGACCCCTGGCCCCGGGGCAAGGTCAACGATCCCC
 ACGGACAGCCCAGGTCTCCGGGTCTGAGTCTCCGG TCTGAGATCCACCCC GAGG CTGGGGACCT G

AEX3F-2

A Locus
 AGACCCTTGHCCTGGAGGGCCAGGGCCCTTWACCCGGTTCA~~T~~TTCA~~G~~TTTAGGCCAAAAAATYCCCCCRGGTTGGTYGGG
 GCBGGR CRGGC TYGGGG ACYGGGCTGAC

yB3F-2a/b/c
 B Locus CCCARACCCCTCGACCGRMGAGGCCAGGGCRCSTTTACCCCCGGTTTCA~~G~~TTCA~~G~~TTCA~~G~~TTCA~~G~~TTCA~~G~~AA
 TCCCGCGGGTTGGTGGGGGG CGGGC (GGGG) TCGGGGG (G) ACKGKGCTGAC
 C Locus CCCAGACCCCTCGRCCGGAGAGGCCYAGTCRCCTTTACCCCCGGTTCA~~G~~TTCA~~G~~TTCA~~G~~TTCA~~G~~AA
 TCCCGCGGGTTGGTGGGGGG TCGS
 E Locus CCCAGACCCCTAGACCCGGAGAGTCTCAGGGCCCTTACCCCCGGG TTCTTTTCAGTTAGGCCAAA
 TGCCACAGGGTGGGGGGGGG TTGGTGG GCGGGACTGAC
 F Locus CCCAGACCCCTCACCCGGAGAGTCCAGGGGGGGG TAGCTGG GCGGGGCTGAC
 TCCCCGGGGTTGGGGAGGGGGG TAGCTGG GCGGGGCTGAC

G Locus	CCCAGACCCCTACTACCTGGAGAACCCCAAGGGCCTTAC	AAAA
	TCCCYGGGGTGGTCGGGGGAGGGAGGG	TCGGTGG GCGGGGCTGAC
H Locus	CCGAGACCCCTTGACCTGGAGAGGGCCCTTACCCGGTTTCATTTCAGTTAGGCCAAA	
	TCCCCGGGTTGGTCGGGGC	TGGGGG ACCGGGCTGAC
J Locus	CAGAGATCCTCGACCCGGAGAGCCCCAGGGGG	TACCTGGTTTCATCTTCAGTTAGGCCAAA
	TCTCCGCAGGGTGTAGGGKCCGGCCAGGGC	TGGTGG GCGGGGCTGAC
K Locus	CCAGATCCTCGACCCGGAGAGGGCCAGGGGG	TCCCGTTAGGCCAAA
	TCCCCGGGTTGGTCGGGGGGGGGGC	TGGTGG GCGGGGCTGAC
L Locus	CCCAGACCCCTCGACCAGGGAAAGAAACTCGGGG	TACCCGGTTAATTTCAGTTAGGCCAAA
	TCCCCGGGGTTGGTCGGGGGGGG	TCGGTGT TCGGGGCTGAC

A Locus	CKYGGGGTCSRGGCCAG	
B Locus	CCGRGGS CKRGGCCAG	
C Locus	CRCGGGSCGGGGCCAG	
E Locus	TAAGGGCGGGCCAG	
F Locus	TGCGGGGACCCGGCTAG	
G Locus	CGARGGGTGGGGCCAG	
H Locus	CGC GGGGGGGCCAG	
J Locus	CGCGGGAACTGGGCCAG	
K Locus	CGCGGGCGGGGCCAG	
L Locus	GGCGGGGGCGAGGCCATG	

Exon 3 Consensus Comparisons

A Locus		
B Locus		
C Locus		
E Locus	GG TCT CAC ACC CTG CAG TGG ATG CAT GGC TGC GAG CTG GGG CCC GAC RGG CGC	
TTC CTC CGC GGG TAT GAA CAG TTC GCC TAC GAC GGC AAG GAT		
F Locus		
G Locus	GT TCT CAY ACC CTC CAG TGG ATG ATT GGC TGC GAC CTG GGG TCC GAC GGW CGC	
CTC MTC CGC GGG TAT GAA CAG TAT GCC TAC GAT GCC AAG GAT		

H Locus GT TCT CAC ACC ATG CAG GTG ATG TAT GGC TGC GAC GTG GGG CCC GAC GGG CGC
TTC CTC CGC GGG TAT GAA CAG CAC GCC ACG CAG ATT CAT
J Locus GG TAT CAC ATC CTC CAG GGA ATG TTT GGC TGC GAC CTG GGG CCC GAC GGG CGT
CTC CTC CGC GGG TAT GAG CAG THT GCC TAC GAC GCC AAG GAT
K Locus
L Locus

A Locus
B Locus
C Locus
E Locus TAT CTC ACC CTG AAT GAG GAC CTG CGC TCC TGG ACC GCG GTG GAC ACG GCG GCT
CAG ATC TCC GAG CAA AAG TCA AAT GAT GCY TCT GAG GCG GAG
F Locus
G Locus TAC CTC GCC CTG AAC GAG GAC CTG CGC TCC TGG ACC GCA GCG GAC ACT GCG GCT
CAG ATC TCC AAG CGC AAG TGT GAG GCG GCC AAT GTG GCT GAA
H Locus GCT CTG AAC GAG GAC CTG CGC TCC TGG ACC GCG GCG GAC ATG GCA GCT
CAG ATC ACC AAG CGC AAG TGG GAG GCG GCC CGT CAG GCG GAG
J Locus TAC ATC GCC CTG AAC GAG GAC CTG CGC TCC TGG ACC GCC GCG GAT ACC GCG GCT
CAG ATT ACC CAG CGC AAG TAT GAG GCG GCC AAT GTG GCT GAG
K Locus
L Locus

A Locus
B Locus
C Locus
E Locus CAC CAG RGA GCC TAC CTG GAA GAC ACA TGC GTG GAG TGG CTC CAC AAA TAC CTG
GAG AAG GGG AAG GAG ACG CTG CTT CAC CTG G
F Locus
G Locus CAA AGG AGA GCC TAC CTG GAG GGC ACG TGC GTG GAG TGG CTC CAC AGA TAC CTG
GAG AAC GGG AAG GAG ATG CTG CAG CGC GCG G

H Locus CAG CTG AGA GCC TAC CTG GAG GGC GAG TTC GTG GAG TGG CTC CGC AGA TAC CTG
GAG AAC GGG AAG GAG ACG CTG CAG CGC GCG G
J Locus CAA AGG AGA GCC TAC CTG GAG GGC ACC TGC ATG GAG TGG CTC CGC AGA CAC CTG
GAG AAC GGG AAG GAG ACG CTG CAG CGC GCG G
K Locus
L Locus

Intron 3 Consensus Comparisons

A-Ex3R-3

A Locus GTACCRGGGCCACGGGGCCCTHCCCTG
ATCGCCTRTAGRTRCTCCGGGCTGGCCTCCCACAGGAGGGAGACAATTGGGACCAACACTAGAATATCRCCCCTCTGGT
CTGAGGGAGGG

B-Ex3R

B Locus GTACCAGGGCAGTGGGAGGCCTTCCCC
ATCTCCTATAGRTRCTGGCCSGGGATGGCCTCCMACGAGAAGRGRGAGGAAAATGRGAKMAGCGCTAGAATGTGCCCTCCSTTGAAT
GGAGAAATGGCATG
C Locus GTACCARGGGCAGTGGGGAGGCCTTCCCC
ATCTCCYRTAGATCTCCGGSATGGCCTYCCACGGAGGGAGGAAAATGGGATCAGCRCTRGAATATCGCCCTCCCTTGAAAT
GGAGAAATGGSATG
E Locus GTAAGAGGGTCCACAGGGCTACTCTCCC
ATCTCCTCTGGCTTAGGACTGTGCCAACAGCTGACAGACCTCAAACAGTAGAAGAACAGGGATGGAGGCCAGAAATTACCACT
CCTCCCTTGATC

F Locus GTACCAGGGCCAT GGGGCCCTCCCT
ATTCCTGAGATCTTGGATGGCCTGGCACAAAGGTTGGGAGGAAGTGGRCCCAATGCTTAGGATATGCCCTCCCTAGT
CTTGAGTGAAG

G Locus GTACCAGGGCAGT
GGGGCCCTCCCTGATCTCCTGTAGACCTCYCAGCCTGGCCTAGCACAAAGGAGAGGAAAATGGGACCAACACYAGAATAATC
GCCCTCCCTCTGGTCCCTGAGGGAGGG

H Locus GTACCAGGGCCACAGGG
CGCTCCGGATGCCCTGTAGATCTCCGGCTGGCTGGCTCCACAAAGAAAGGAGACAAATGGGACCAACACTATAATATCGCCC
TCCCTCTGGTCCCTGAGGGAGGG

J Locus GTACCAGGGCCAT
GGGAGGCCTGCTCGATCTCTGTAGATCTCCGGGCTGGCTCGCACAAAGGAGGGAAAGAAAATGGAAAMCACCAGAACATAATC
GCCCTCCCTCTGTGACGGAGGG

K Locus GTACCAGGGAACACAA
GACGCCCTCCCTGATGCCCTGTAGATCTGGGCTGGCTTCCCACAAAGAGAAAGGAAAATGGGACCAACACTAGAAATGTCGT
CCTCTCTGGTCCCTGAGGGAGGG

L Locus GTACCAGGGCCACGGGAGGG
CAATGCTAGAAATGCCCTCCCACTGGTCCGTGAATGGGAAG

A Locus AATCCTGGTTCCAGATCCCTGTACCCAGAGGAGGTGACTCTGAGGGTCCGS CCTGCTSTGAC
WCAATTAAAGGGATAAAATCTCTGAMGGARTGACSGRAAGACGA TCCCTCGAATACTG
B Locus AGTTTCCCTGAGTTCC
CCCCCTKCTSTCTAG (G) ACAATTAAAGGRATGACRTCTCTGAGGAATGKAGGGAAAGACAGTCCCTAKRATASTG
C Locus AGTTTCCCYGAGTTCC
ACAATTAAAGGGATGAAGTCYYTGAGGAATGGAGGAAAGACAGTCCTRGAAATACTG
E Locus AGGAGGGAGCTGTCAACCTGAGGTACAGGAGATCCTATAACACAGAGTGACTCTTAA
GGCCAGACCTCTCAGGGCAATTAGGAATCTAGTCTCGCTGGAGATTCCATCCTCAGAT
F Locus AATCTTCCCTGGCTTTGGAGATCCGGTACCAAGAGGTGACTGTGAGAGTCCGCCCTGCTCT
GGGACAATTAAAGGGATGAATYTYCTGAGGAATGGAGGG AAGACAGTCCCTGGAAATACCGATC
G Locus AATCCTCCCTGGTTTCCAGATCCCTGTACCAAGAGGTGATTCTGAGGGYCCGTCCCTGCTCT
GGGACAATTAAAGGGATGAAGTCTGAGGGAGTGGAGGGAAAGACATACTGGGARGACTGATC
H Locus AATCCTCCCTGGTTCCA
GACACAATTAAAGGGATGAATCTGTAGGAATGAAGGG AAGACATCCCTGGAAATACTGATG

J Locus
AATCCTCCTGGTTCCAGATCCTGTATCAGAGATTGACTCTGAGGGCCACCCCTGCTTCCGGACAATTAAAGGGATGAAG
TCTCTGAGGGAGTGAGGGGAAGACAATTCCCTGGAGACTGATC
K Locus
AATCCTCCTGGTTCCAGATCCTGTACAGAGAGGTGACTCTGAGGGTCTGCCCTGCTCTC
TGATACAATTAAAGGGATGAAATCTGTAGAGAAATGAAGGG AAGACAATTCCCTGGAAATACTGATC
L Locus
AATCCT TGTTCCAGATCCTGTACAGAGAGTAACCTGTAGAGCCCACCCCTGCTCTC
TGGACAAATTAAAGGGATGAAAGTCCTGAGGAATGGAGGAAGACAGTCCCTGGAAATACTGATC

PA3-31

A Locus ATGASTGGTCCCTTG (CAC)
CCGTGACTTTCCCTCAGGCCCTTGTCTGCTTCACACTCAATGTTGAGTCCAGCAC
PB 3-24

PB5-55+4

CTGCAGCAGGCC

GGMACCRTGACTTTCYTCTAGGCCCTTGTCTGCTCTGCCYCACACTCAGTGTGGGGCTCTGATTCAGCAC

PB 3-24

C Intron 3 R

C Locus ATCAGGGGTCTGTCTGCCTTSAYRCTCAATGTGTYTRAAGGTTGAYTCCAGCT
TCTCAGGCCCTTGTCTGCCTTSAYRCTCAATGTGTYTRAAGGTTGAYTCCAGCT
E Locus GAACTGATGAGCAGTTCTCTT

GACTCCCAGTATTAGGAATCACGGGGAGTTGAGTTCTCGTGCCCTGATCTCAGCCCCACACCAAGAGTTTGGAGGTTCTGACTC
CAGCTTTCTCAGTCAC
F Locus CGGGTCCCTTGAGGCCCTCCAACAGGCCCTGGGCCCGTGACTIONTCTC
TCAAGTTTGTCTGCCTCACACTCAATGTGTTGRRGGCTCTGATTCCAGTCCCTGGGCTCCACTTAGGTCA
G Locus AGGGGTTCCCTTGACCCC ACAGCAGGCCCTGGCACCCAGG ACTTTCCCC
TCAGGCCCTTGTCTGCCTCACACTCAATGTGTTGGGRGCTGACTCCAGCTCCCTGGGC
H Locus AGTGGTTCCCTTGACACTGGCAGCTGG
ACTTTCCCTCAGGCCCTTGTTCAACACTCAATGTGCTCTGCTGAGTCCAGCTCTGAGTCCT
J Locus CGGGTCCGGGCTTCAACCC ACAGCAACCTTGGAACCCAGG CCCGTG
ACTTTCCCTCAGGCCCTTGTTCAACACTCAATGTGCTCTGCTGAGTCCAGCTCTGAGTCCT
K Locus AGGGGTTCCCTTGACACAGGAGGCCCTGGGGCTCTGAGTCCAGCTCTGAGTCCT
AGGCCCTTGTCTGCCTTACACTCAATGTGTTGGGGCTCTGAGTCCAGCTCTGAGTCCT
L Locus CGTGGTCCCTTGACCCCTGAGCCCTGGCACCCAGGAATTTCCTCT
AGGCCCTTGTCTCCCTCACACTCAGTGTCCGTGGCTCCGATTCCAGCTCTGAGTGCCTGGC

pA5-5

A Locus TTCTGAGT CYYTCA GCCTCCACTCAGGTCAAGGCCAGAAAGTCGGCTGTTCCCTYTCAGGGA
(CTAGAATTTCACCGGA) ATAGRAGATTATCCCAGGTGCTGTGGCTGGGTGCT
B Locus TTCTGAGTCACTTA CCTCYACTYAGATCRGGAGCAGAACGTCYCTGTTCCCCRCTCAGAGA
CTCGAACATTCCAATGA ATAGGAGATTATCCCAGGTGCTGYRTCCAGGGCTGGTGTHT
C Locus TTHTGAGTY CTK CR GCCTCCACTCAGGTCAAGGACCAGAAAGTCGGCTCAGAGA
CTAGAACTTCCAAGWA ATAGGAGATTATCCCAGGTSCCTGTGTCCAGGGTGGCCT
E Locus AGCATCCACACAGGCCAGGACCAGAAATCCCTTTCAACCTCTACCTGGGCTAGCTCATCCGGATTCTAGAAC
TTTCCAAGGA ATAAGAGGCATATCCCAGATCCCTTAAGTCCAGGCTGGTCA
F Locus GGGCCAGAAGTCCCTGCTCCCCVCTCAGAGACTCKAACTTCCAAGGAATAGGAGAT
TTTCCAGGTGTC
G Locus CTCCCACTCAGGTCAAGAACRGAGGTCCCTGCTCCCCGCTCAGAGA
CTAGAAC TTTCCAAGGAATA GGAGATTATCCCAGGTGCCCGTGTCCAGGGCTGGTGTCA
H Locus CAGCCTCCACTCAGGTCAAGGACCAGAACGTCGGCTGTTCCCTCAGGACTAGAA
TTTCCACGGAAATA GGAGTTATCCCAGGTCTGGGTGTCAGGTGTTGCT
J Locus CTCCCACTCAGATCAGG CCAGAASTCCCTGCTAACCTGCTCAGAGA
CTAGAAC TTTCCAAGGAATA GGAGATTATCCCAGGGGCCCTGTGTCAGGCTRGTTGCT
K Locus CTCCCACTCAGGTCAAGGACCAGAACGTCAGGTGCTGGGAA
CTGGAATTCCACGGAAATTGGAGATTATCCCAGATAACCTGTGTCAAGGTGGTGTCT
L Locus CTCCCACTCAGGTCAAGGACCAGAACGTCAGGTGCTGGGAA
CTCGAACATTCCAAGGAATA GGAGATTATCCCAGATTCCAGGTGGTGTCT

Aex4F

A Locus GGGTCTGTGCTCYCTTCCCCATCCCCRGGTGTCCCT GTCCATTCTCAAGATRGCCACATGYR TGCTGG W
GGAGTGTCCCATKACAGATSSAAAATGCCTGAATKWTCTGACTCTCCYG WSAG
B-Ex4F1
B Locus GGGTCTGTG YCCCTTCCCCACMCCAGGTGTCACATGGG TGGCCCTA
GGGTGTSCYATGARAGAT GCAAAGGCCCTGAATTCTGACTCTCCCATCAG

C Locus	GGGTCTGCCSCTTYCCYACCCCCAGGGTGTCTT GGAGTGTCSAAGAGAGAT	GTCCRTTCTCAGGATRGTCACATGGG	CRCTGYT
E Locus	AGTTTTGTCCCTCTTCCT ACTATAATTGTCCTCT GGAGTGTCCCATGAGAGAT ACAAAAGTGCCTGAATTTC	TTCTCAGGATGGTCACATGGG	TGCTGCT
F Locus	GGGTCTGTGTCCTCCCCACCCCAGGGTGTCT GGGGTTCCATGAGAGT GCAAAGTGCCTGAATTTC	TCCAKTCTCAGGTTGGTCACATGGG	TGCTGCT
G Locus	GGGTCTGTGTCCTCCCCACCCCAGGGAT CTGGTTCAT GGAGTGTCCCATGAGAGAT GCAAAGTGCCTGAATTTC	CTGGTTCATCTTAGGATGGTCACATCCAGGTGCTGCT	TGCTGCT
H Locus	GGGTCTGTGTCCTCCCCACCCCAGGGTGTCT GGGAGTGTCCCATGACAGAT GCAAATGCGCTGAATTTC	GTCCATTCTCAAGATGCCCACATGGC	TGCTGG
J Locus	GGGCTCTGTGTCCTCCCCACCCCAGGGTGTCTTA GGTCCCATGAGGAAT GCAAAGTGCCTGAATTTC	TTCATCAGGATGGTCACATGGGCC	TGCTGG
K Locus	GGGTCTGTGTCCTCCCCACCCCAGGGTGTCT GGAGTGTCTCATGAGAGAT GCAAAGTGCCTGAATTTC	GTCCATTCTCAGGATGCCCACATGGC	TGCTGCT
L Locus	GGGTCTGTGTCCTCCCCATGCCAGGGTGTCT GGAGTGTCCCATGAGGAAT GCAAAGTGCCTGAATTTC	GTCCATTCTCAGGATGGTCACATGTA	TGCTGCT

Exon 4 Consensus Comparisons

Intron 4 Consensus Comparisons

E Locus	GTA	AGG	AGG	GGG	ATG	GGA	GGT	CAT	GTC	TCT	TCT	CAG
T TC T	GTA	AGG	AGG	GAG	ATG	GG	AG	CC	CTT	C	CG	CAG
F Locus	GTA	AGG	AGG	GAG	ATG	GGT	AAA	G	AG	GGG	AAC	GAG
TG TC T	TTT	C	TCA	GGG	AAA	GCA	GG	AG	CC	CTT	C	TG
G Locus	GTA	AGG	AGG	GAG	ATG	GA	GGC	AT	CAT	GTC	TGT	GAG
TC TC T	GTA	AGG	AGG	GAG	ATG	GA	AG	AC	CTT	TA	ACA	CC
H Locus	GTA	AGG	AGG	GAG	ATG	GGG	GTG	T	CAT	GTC	CCT	GAG
TC TC T	GTA	AGG	AGG	GAG	ATG	GG	AG	AG	CTT	TA	GCA	CC
J Locus	GTA	AGG	AGA	GAG	ATG	GGG	GCG	GC	CAT	GTC	TCT	TAG
C TC T	GTA	AGG	AGG	GAG	ATG	GG	AG	AC	GG	AG	AAG	GAG
K Locus	GTA	AGG	CAG	GAG	CTG	AGT	GGA	GGG	GTC	ATG	TCT	CTT
C TC T	GTA	AGG	CAG	GAG	CTG	AGT	GGG	GGG	GTC	ATG	A	GAG
L Locus	GTA	AGG	AGG	GGT	GTA	AGT	T	GG	AG	AA	CTT	C AG
AC CTT C AG	CAG										GTC	TCC

A Locus	CCT	TCC	CCT	CTT	TTC	CCA	G				GGT	CAG	GGC	CCC	TCA
B Locus	TCC	CYT	CCT	TTC	CCA	G					GGT	CRG	GRC	CCC	TCR
															C3API4T/C/TAC
C Locus	TCY	CCT	CCT	TTC	CCR	G					GGT	MAG	GGC	CCC	TCA
CCT	TCY	CCT	CCT	TTC	CCR	G					GGT	CAG	GGC	CCC	TIA
E Locus	TCC	CCT	CTT	TTC	CCA	G					GAT	CAG	GGC	CCC	TCA
CGT	TCC	CCT	CTT	TCA	GGG	TCA	G				GAT	CCT	GGA		
F Locus	CTC	CTC	T	TCA	GGG	TCA	G				GAT	CAG	GGC	CCC	TCA
CCT	TCC	CTT	CCT	TTC	CCA	G					GAT	CAG	GGC	CCC	TCA
G Locus	TCA	CCT	CCT	TTC	CCA	G					GAT	CAG	GGC	CCC	TCA
CCT	TCA	CCT	CCT	TTC	CCA	G					GAT	CAG	GGC	CCC	TCA
H Locus	TCC	CCC	CRT	TTC	CCA	G					GAT	CAG	GGC	CCC	TCA
J Locus	TCC	CCC	CRT	TTC	CCA	G					GAT	CAG	GGC	CCC	TCA
CAT	TCC	CCT	CCT	TTC	CCA	G					GAT	CAG	GGC	CCC	TCA

K Locus		GG TCG GTG CTG	GGG GCT GAG	GGT CAG GGA CGC TCA
CCT TCC CCT	TTT TTC CCA G			
L Locus	GG CA GGG CTG	AGG CCT GGG	GGT CAG AAC CCC TCA	
CCT CC CTC T CCT TTC CCA G				

Exon 5 Consensus Comparisons

A Locus	AG CYR TCT TCC CAG CCC ACC RTC CMC ATY GTG GGC ATC MTT GCT GGC CTR GTT CTC			
YTT				
B Locus	AG CCR TCT TCC CAR TCC ACC RTC CCC ATC GTG GGC ATT GTT GCT GGC CTG GCT GTC			
CTW				
C Locus	RG CCR TCT TCC CAG CCY ACC ATC CCC ATC RTG GGC ATC GCT GGC CTG GCT GTC			
CTG				
C 170*	AG CGG TCT TCC CAG CCC ACC ATC CCC AAC TTG GGC ATC GTT TCT GGC CCA GCT GTC			
CTG				
E Locus	AG CGG GCT TCC CAG CCC ACC ATC CCC ATC GTG GGC ATC ATT GCT GGC CTG GTT CTC			
CTT				
F Locus	AG CAG TCT CCC CAG CCC ACC ATC CCC ATC GTG GGC ATC GTT GCT GGC CTT GTT GTC			
CTT				
G Locus	AG CAG TCT TCC CTG CCC ACC ATC CCC ATC ATG GGT ATC GTT GCT GGY CTG GTT GTC			
CTT				
H Locus	AG CCA TCT TCC CAG CCC ACC ATC CCC ATC GTG GGC ATC GTT GCT GGC CTG GTT CTA			
CTT				
J Locus	AG CCC TCT CCC CAG CCC ACC ATC CCC ATT GTG GGT ATC ATT GCT GGC CTG GTT CTC			
CTT				
K Locus	AG CAG TCT TCT CAG CCC ACC ATC CCC ATC GTG GGT ATC GTT GCT GGC CTG GTT CTC			
CTT				
L Locus	AG CGG TCT TCT CAG CCC ACC ATC CCC ATC GTG GGC ATC GTT GCT GGC CTG TTT CTC			
CTT				

GCC ATC ACA GCT CCT AGG ACA GCT A

A Locus	GSA	GCT	RTG	RTC	RCT	GGA	GCT	GTG	GTC	GCT	GCY	GTG	AKG	TGG	AGG	ARG	AAS	
AGC TCA	G																	
PA3-29																		
B Locus	GTG	GYM	RYY	GTR	GYX	RTS	GKM	GCT	GTG	GTC	GCT	RCT	GTG	RTG	TGT	AGG	AGG	AAG
AGY TCW	G																	
PB3-20, 21, 22, 23																		
C Locus	GYT	GTC	CTA	GCT	GTG	CTW	GGA	GCT	RTG	RTS	RCY	GYT	RWK	ATG	TGT	AGG	AGG	AAG
AGC TCA	G																	
C 170*	GCT	GTC	CCG	GCT	GTC	CTG	GCT	GTC	CTA	GCT	GTC	GTC	GCT	GTC	GTC	GCT	GCT	GCT
GTG ATA	C																	
E Locus	GGA	TCT	GTG	GTC	TCT	GGA	GCT	GTG	GTT	GCT	GCT	GTC	GTG	ATA	TGG	AGG	AAG	AAG
AGC TCA	G																	
F Locus	GGA	GCT	GTG	GTC	ACT	GGA	GCT	GTG	GTC	GCT	GCT	GTC	GCT	GTG	ATG	TGG	AGG	AAG
AGC TCA	G																	
G Locus	GCA	GCT	GTA	GTC	ACT	GGA	GCT	GCG	GTC	GCT	GCT	GTC	GCT	GTG	CTG	TGG	AGR	AAG
AGC TCA	G																	
H Locus	GTA	GCT	GTG	GTC	ACT	GGA	GCT	GTG	GTC	GCT	GCT	GTC	GTA	ATG	TGG	AGG	AAG	AAG
AGC TCA	G																	
J Locus	GGA	GCT	GTG	GTC	ACT	GGA	GCT	GTG	GTC	ACT	GCT	GTC	ATG	TGG	AGG	AAG	AAG	
AGC TCA	G																	
K Locus	GGA	GCT	GTA	GTC	ACT	GGA	GCT	GTG	GTT	TCT	GCT	GTG	ATG	TGC	AGG	AAG	AAG	
AAC TCA	G																	
L Locus	GGA	GCT	GTG	GTC	ACT	GGA	GCT	GTG	GTT	GCT	GCT	GCG	ATG	TGG	AGG	AAG	AAA	
AGC TCA	G																	

Intron 5 Consensus Comparisons

A Locus GTGGRG (TG) AAGGGRGTAARGGTGGGTCTGAGGATTCTGTCACTGAGGGTCCAAAGMCCCAGSTAGAARTGTGCCCTGY
 CTCRTTACTGGGAAGGCACCDYCCACAATYATGRGCCKACCC

B Locus GTAGGG
 AAGGGGTGAGGGGTCTGRGTTYSTTGTCCACTGGGGTTCAAGCCCCAGGTAGAACGTTACTG
 GGAWGCAGCATSCACACA GGGGCTAAYG
C Locus GTAGGG
 AAGGGGTGAGGGGTCTGGGTTTCTTGTCCACTGGGAGTTCAAGCCCCAGGTAGAACGTTACTG
 G AGGCACCATCCACAC Y TGGGCCATCCC

E Locus GTGGGG
 AAGGGGTGGGGTCTGAGTTTCTGTCCCACTGGGTGTTCAAGGCCCTAGGTAAAAGTGTGCTCGTTACTGGAAAGCA
 CCATCCACACACAGGCCCTACCC

F Locus GTAGG
 AAGGGGTGAGGGAGTGGAGTCTGAGTTCTTGTCCACTGGGGTTGCAAGCCCCAAGTAGAACGTTACTG
 GGAAGCACCACATCCACACTCATGGGTCTACCC

G Locus GTAAGG
 AAGGGGTGACAAGTGGGGTCTGAGTTCTTGTCCACTGGGGTTCAAGCCCCAGGTAGAACGTTACTG
 GGAAGCACCACATCCACACTCATGGGCCTACCC

H Locus H
J Locus GTGGGG
 AAGGGGTGAGGGAGTGGGGTTGAGTTCTTGTCCACTGGGGTTCAAGCTCCAGGTAGAAATGTGTTCTGCCTGGTTACCG
 GGAAGCACCACATCCACATTCATGGGCCTACCC

K Locus K
L Locus L

A Locus AGYCTGGG CCCTGTGTGCCAGCACTTACTCTTTGTAAAGCACCTGT
 AMAATGAAGGGACAGATTATCACCTT GATTAYRGCRTGATGGACCTGTATCCAGTCACAGTCACAGGGG
B Locus AGMCTGGGACCCCTGTGTGCCAGMACTTACTCTTTGTGCAGCACATGTG
 ACAATGAARSAYRGATGTATCRCCCTTRTGGTTGTGGTGTGGGTCTGATTYCAGCATTCAATGAGTCA GGGG
C Locus AGCCTGGGACCCCTGTGTGCYAGGCACTTACTCTKTGTGAAGGCACATG (TG) ACAAYGAAGGACRGATGTATCACCTT
 GATGATTATGGGTGGGTCCCTGATTCAGCATTCRTGAGTCAGGG

E Locus
 AGCCTGGGGCCCTGTGCCAGCACCTACTCTTTGAGACGGAGTCTGGCTCTGTCACCCAGGCTGGAGTCATGGC
 GTGGTTCAAGCTCACTGCAACCTCGGCCTCCCCAGGTCAA

F Locus
 AGCCTGGG CCCTGTGCCAGCACCTACTCATTTGTAARGCTCTG TG
 AAAATGAAGGACAGATTCTTCAC TTGGATGATTATGGGGATGGG ACCTGATCCCAGCAGTCACAAT

G Locus
 AGCCTGGG CCCTGTGCCAGCACCTCTCTAAAGCACCCTG TG
 ACAATGAAGGACAGATTATCACCTT GATGATT GTAGTGATGGGACCTGATCCTAGTAATCAC

H Locus

J Locus
 AGCCTGGG CCCTGTGCCAGCACCTACTCTTTGTAAG GCACCTG TG
 ACAATGAAGGACAGATTCTCACCTT GATGATT GTAGTGATGGGATCTGACCCAGTAATCAC

K Locus

L Locus

A Locus
 AAGGTTCCCC TGAGS
 ACAGACYTCAGGGGGCKRTTGGTCCAGGRCCCACAYCTGCTTTCTCATGTTCCCTGATCCYGCCCTGGGTCTGCAGTCACAC
 ATTTCCTGAAACT

B Locus
 AAGGTTCCCTGCTAAGG
 ACAGACCTTAGGGGGCAGTTGGTCCAGGACCCACACTTGCTTTCCCTYGTGTTCCCTGATCCTGGGTCTGTAGTCATACT
 TTCTGGAAATT

C Locus
 AAGGTTCCCTGCTAAGG
 ACAGACCTTAGGGGGCAGTTGSTIYCAGRACCCACARCTGCTTTCCCYRTGTTCCCTGATCCTGGGTCTGCAGTCR
 TAGTTCTGGAAACT

E Locus
 GCAATTCTCCTGCCCTCAGGCCCTAGTAGTGGGACTACACATGCCACACCTGGCTAATTTTTTGGTATT
 TAGTGGAGATGGGGTTCACTATGTTGGCCAGGCTGGTCTCGAACT

F Locus
 CACAGGGGAAGGTCCCTGCTGATG
 ACAGACCTCAGGGGGCAGTTGGTCCAGGACCCACATCTGCTTTCTCATATTCTGATCCTGGATCTACAGTTACAC
 TTTCTGGAAAC

G Locus
 AGGTAGGGAAAGGTCCCTGGCTAAGGACAGACCTAGGAGGGCAGTTGGTGGAGGACCCACATCTGCTTTCCCTGTTTCCT
 GATCCCGCCCTGAGTCTGCAAGTCACACATTCTGGAAAC

H Locus

J Locus AGGTCAAGGGAAAGGTCCCCTGCTGA
GGACAGACCTTAGGAGGGCAGTTGGTCCAGGACCCACATCTGCTTCCCTTGTTTYCCTGATCCTGCCCTGGTTGCAGTCAC
ACATTTCCTGAAAC

K Locus

L Locus

A Locus TCTCTGRGGTCCAAGACTWGGAGGTTCCCTAGGACCTTAAGGCCCTGRCTCYTTCTGGKATCTCACAGGACATTTCCTTCYC
ACAG

B Locus CCTTTGGKTCCAAGACKAGGGTTCCCTAAGATCTCATGGYCCCTGCTTCCAGTSCCCCTCACAGGRCATTTCCTTCCC
ACAG

C Locus TCTCTGGGTCCAAGACTAGGAGGTTCCCTAAGATYRCATGCCCTGMCTCCCTCCWGTCCTCAYAGGGCATTTCCTTCCC
ACAG

E Locus CCTGACTTTGTGATCTGCCTCGGCCTCCCAAAGTGTGGATTACAGTCGTGACCACCCAGCCACCGCACCTACTCT
TTTGTAAGACACTGTGACAATGAAGGAAGAACAGATTATCACCT

F Locus TTCTCTGGGATCAAAGACTAGGGGTTGCTCTAGGACCTTATGCCCTGCCTCCTCACAGGACATTTCCTTCCC
CATAG

G Locus TTCTCGAGGGTCCAAGACTAGGAGGTTCTAGGACCTCATGCCCTGCCACCTTCTGGCCTCTCACAGGACGTTTCCTTCCC
CACAG

H Locus

J Locus TTCTCRAGGGTTCCAAGACTAGGAGGTTCTAGGACCTCATGCCCTGCCTACAGGACGTTTCCTTCCC
CGCAG

K Locus

L Locus

A Locus

B Locus

C Locus
E Locus
TGACGATTGGGTGATGGGGACCTGATCCCAGCAGTCACAGGTACAGGGAAAGGTCCCTGCTGAAGACAGACCTCAGAAAGGGC
AGTGTGATCCAGGACCCACACCTGCTTCACTGTTTCCCTG
F Locus
G Locus
H Locus
J Locus
K Locus
L Locus

A Locus
B Locus
C Locus
E Locus
ATCTGCCCTGGGTCTGCAGTCAGGAAACTTCAGGATCCA
AAACTAGGAGGTCCCTCTAGGACCTTAGGGCCCTATGGCCCT
GCCTCCCTGGCCCCCTCACAG
F Locus
G Locus
H Locus
J Locus
K Locus
L Locus

A Locus	WT AGA AAA GGA GGG AGY TAC WCT CAG GCT GCA A
B Locus	GT GGA AAA GGA GGG AGC TAC TCT CAG GCT GCG T
C Locus	GT GGA AAA GGA GGG AGC TGC TCT CAG GYT GCG T
E Locus	GT GGA AAA GGA GGG AGC TAC TCT AAG GCT GAG T
F Locus	AT AGA AAC AGA GGG AGC TAC TCT CAG GCT GCA G
G Locus	AT TGA AAA GGA GGG AGC TAC TCT CAG GCT GCA A
H Locus	AT AGA AAA GGA GGG AGC TAC TCT CAG GCT GCA A
J Locus	AT AGA AAA GGA GGG AGC TAC TCT CAG GCT GCA A
K Locus	AT AGA GTG AGC TAC TCT GAA GCT GCA A
L Locus	AT AGA ACA AGG AGC TAT GCT CGG GCT GCC T

Intron 6 Consensus Comparisons

A Locus	GTAAGTATGAAGGAGGAGTGTSCMWGARRTCM YTGGGATATGTGTTGGAGCCCRTGGGGAGCYCAMCCA CCYCACACAATTCCCTAGGCCACATSTTCTGTGGGATCT GACCAGGTTTC	
B Locus	GTAAGTGTGGGGYGGGA CCCCATAATTCCCTCTGT CMCACGTCCTGGCTCTTGACCAGGTC	
C Locus	GTAARTGATGSCRGYRGCC YACCYA CYCCATAAYTCCTCTGT CCCACATCTCCCTGGGGCTCT GACCAGGTCTT	
E Locus	GTAAAGTGC AATTCCCTGCA CCACATCTCCCTGGGCTCTGACCAGGTCT F Locus	GGGGGGGAGGCT GTAAGATGAAGGAGGCTGATCCCTGAGATG TTGGGATATGTGGTCAGGAGCCTATGAGGGAGCTCACCCA CCCCACAGTT CTGGGCTCTGACCAGGTCC
G Locus	GTAAGTATGAAGGAGGCTGATCCCTGAGATCC TTGGGATCTGTGTTGGAGCCATGGGGAGCTCACCCA CCCCACAATTCCCTCCCTGCCCCACATCTCCCTGTGGTCTGACCAGGTGC	

H Locus	GTAAGTATGAAGGAGGTGATCCCTGAATCCTTTGG ATATTGTGTTGGAGCCCCATGGGGAGCTCACCA
J Locus	CCCACAAATTCTTCCTCTAGCCACATCTACTGTGGATCTGACCAGTCC
K Locus	TTGGATATGTGGTGGAGGCTGATCCCTGAGATCC
L Locus	CCCACAAATTCCCTCCTCTAGCCACATGGGGAGCTCACCA
M Locus	TTGGATATGTGGTGGAGCCCCATGGGGAGCTCACCAACCCAGA
N Locus	TTCTCCTCTAGCCGATCTCCCTGGCTCTGACCAAGTCC
O Locus	GTAGATG GGGATTAGGGCTGC TCCC TGAGATCGT TGGACAGTAGACAAGA TTCTCCTTAGCCACATCTCTGGCTCTGACCAAGTCC
A Locus	TGTTTTTGTYCTACCCAG
B Locus	TGTTTTGTTCTACTCCA
C Locus	TTTTTTGTTCTACCCAG
D Locus	TGTTTTGTTCTACCCAG
E Locus	TRTTTTGTTCTACCCAA
F Locus	TGTTTTGTTCTACTCTAG
G Locus	TGTTTTATTCTACTCCAG
H Locus	TGTTTTGTTCTACCCAG
I Locus	TGTTTTGTTCTACCCAG
J Locus	TGTTTTGTTCTACCCAG
K Locus	TGTTTTGTTCTACCCAG
L Locus	TATTTTGTTCTACCCAG

Exon 7 Consensus Comparisons

A Locus	GC AGT GAC AGT GCC CAG GGC TCT GAT RTG TCY CTC ACA GCT TGT AAA G
B Locus	SC AGC GAC AGT GCC CAG GGC TCT GAT GTG TCT CTC ACA GCT TGA AAA G
C Locus	SC AGC AAC AGT GCC CAG GGC TCT GAT GAG TCT CTC ATC RCT TGT AAA G
E Locus	GC AGC GAC AGT GCC CAG GGG TCT GAG TCT C ACA GCT TGT AAA G
F Locus	TC ACT GAC AGT GCC TCT GGG GTG TCT CTC ACA GCT AAT AAA G
G Locus	GC AGT GAC AGT GCC CAG GGC TCT AAT GTG TCT CTC ACG GCT TGT AAA T
H Locus	GC GGC AAC AGT GCC CAG GGC TCT GAT GTG TCT CTC ACA GCG TGA AA G
J Locus	GC AGC CAA AGT GCC CAG GGC TCT GAT GTG TCT CTC ACG GCT TGT AAA G
K Locus	GC AGC GAC CAT GCG CAG GGT TCT GAT GTG TCT CTC ACG GCT TGT AAA G
L Locus	GC AGC AAT TGT GCT CAG TAC TCT GAT GCA TCT CAT GAT ACT TGT AAA G

Intron 7 Consensus Comparisons

A Locus GTGAGAGCYTGGAGGRCTRATGGTGTGGGTGTTGGYRGAACAGTGGACRAGCTGTGCTA
TGGGGTTTCTTTSCRITGGATGTATTGAGCATGGCATGGCAT

B Locus GTGAGATTCTTGGGTCTAGAGTGGYRGGGKGSVKGTCGGKSKKGRKGCCAGWGGGAAAGGCCCTGGTAATGGRSAT
TCTTGATTGGGATGTTTCGGTGTGTSRT

C Locus GTGAGATTCTGGGAGCTGAAGTGGTC
KGGGGTGGGGCAGAGGGAAAAGGCCTRGGTAATGGGATYCTTGTGATTWGGAACGTTTCGARTGTGTTGGT

E Locus GTGAGATTCTGGGGTCTGAAGTGGGTGGGGCAGAGGGACAGGACTGGGTTGTGGGATTTTTGATTCAAATT
TTGAGTGTGGTGGCTAGAGTGTCACT

F Locus GTGACACTCCAGGGCAGGGCCCTGATGTGAGTGGGTGTTGACTGGATGTCATGAAT
GGGGAACTCAGCTGTGCTATTGGTTCTTGACTGGATGTCATGAAT

G Locus	GTGACACCCC	GGGGGCCCTGATGTTGGGGTGTGAGGGV AACAG
BGGACATAGCTGTGCTATGAGGTTCTTGACTTSAATGTTGACATGTGAT		
H Locus	GTGAGACCTT	GGGGGCCCTGATGTTGGGGTGTGGGGGAACAG
TGGACACAGCTGTGCTATGGGG TTCTTGAAATTGATGTTTGACATGCGAT		
J Locus	CTGAGACCCCT	GGGGAGGCTGATGTTGGGTGTTGGG TAACAG
TGGATATAAGCTGTGCTATGGGGTTCTTGACTTGGATGTTCAACATGAT		
K Locus	GTGAGACACT	GGGGGACCTGATGTTGGGGGTGTTGGGGC AATAG
TGGACGCAGCTGTGCTATGGGGTTCTTGAAATTGGATGTTGACATGTGAT		
L Locus	GTGAGACAT	GGGGGGCCCTGAAGT GGGGGGTG AGGCAGAGGGGACATGATTCTGTTGA
GGGGTT CTCGGATTAGACAT		

A Locus	GGGCTGTTAARGTGTGACYCCTCACTGTGAYRGATAYGAAKTTGTTCATGAATWTTTTTCTATAG		
B Locus	GGGCYGTYYAGASTGTCATCRCTTACCATGACTAACCGAAATTTGTTCATGACTGTTGTTCTGTAG		
C Locus	GRRCYGTTCAAGAGTGTSATCRCTTACCATGACTGACCTGAATTTGTTCATGACTATTGTTCTGTAG		
E Locus	ACTTACCGTGAECTGACTGACCTGAATTTGTTCATGACTATTGTTCAATGAATATTCT CTATAG		
F Locus	GGGCTATTAGAGTGTACCTCTACTGTGACTGATACTGAATTTGTTCAATGAATATTCT CTATAG		
G Locus	GGGCTGTTAAAGTGTCAACCCTCACTGTGACTGATATGAATTTGTTCATGAATATTCT TCTGTAG		
H Locus	GGGCTG CCAAAGTGTCACTCCATTAATGGGACAGATATGAATTTGTTCATGAATATTCT TCTATAG		
J Locus	GGGCTGTTGAAGGGTGTGACCCCTCACTGTGAGTGATATGAATTTGTTCATGAATATTCT TCTATAG		
K Locus	GGGCTGTTAAAGTGTCAACCCTCACTGTGACGGATATGAATTTGTTCATGAATATTCT TCTATAG		
L Locus			

Exon 8 Consensus Comparisons

A Locus TG TGA

B Locus	CC TGA
C Locus	CC TGA
E Locus	CC TGA
F Locus	TG TGA
G Locus	TG TGA
H Locus	TG TGA
J Locus	TG TGA
K Locus	TG TGA
L Locus	CT TGA

3' Untranslated Consensus Comparisons

A3'UT	A Locus	GACAGCTGCCTGTGAGGGACYGAGATGCAGG ATTTCCTTCACKCCT CCCCTTTGTGACTTCAAGAGCCCTCT GGCATCTCTTT CTGCCAAAGGCACCTGAATGTGCTGYGTYCCCTGTTAG
CT	GAC	TTTGTTT CTGCAAAGGCACACTGCATGTGTCATGTGTCTGTAGG
B 3' UT		B 3' UT
B Locus		GACAGCTGCCTGTGAGGGACTGAGATGCAGG ATTTCCTTCACKCCT CCCCCTTGTGACTTCAAGAGCCCTCT GGCATCTCTTT CTGCCAAAGGCACCTGAATGTGCTGYGTYCCCTGTTAG
C Locus		GACAGCTGCC TGTGTGGACTGAGATGCAGG ATTTCCTTCACACCT YTCC
TTTGACTTCAAGAGCCCTCT RGGCATCTCTTT CTRCAAAGGCCAYCTGAATGYGTCCTGGTCTGTGTTAG		
E Locus		GACAGCTGCCTGTGAGGGACTGAGATGCAGG ATTTCCTTCACKCCT CACGCCTCCCTATGTGCTTAAGGGACTCTGGCTTCTCTGGCAAGGGCCCTCTGA
F Locus		GACAGCTCCCTGTGAGGGACTGAGATGCAGG ATTTCCTTCACKCCT ATATCAAATGAGCAGATTGCACCTGTGCCTCACGAACATAAAATTAAAATATATCTTTATAGA TACAGGTAG
G Locus		AACAGCTGCCCTGTGAGGGACTGAGATGCCAG (ATT GTTCATGCCT) TCCCTTTGTGACTTCAGAACCCCT
GACTYCTCTT STGCAGAG		ACCAGCCCACCCCTGTGCCAAC
H Locus		GACAGCCGGTCTGTGAGGGACTGAGGGCAAG ATTGTGTTCACACCC T TCCCTTTGTGACTTCAGAACCC
CT	GAC	TTT CTGCAAAGGCACACTGCATGTGTCATGTGTCTGTAGG

J Locus GACAGCTGCCTTGTGTGGGACTGAGAGGCAAG ATTGTTCATGCC T TCCCTTGTGACTTCAGAACCC
CT GACTTCTCTTT CTGCAAAGGCATCTGAATGTGTCTGTGCTTCCCTATAGG
K Locus GACAGCTGCCTTGTGTGGGACTGAGAGGCAAG ATTGTTCACGCC TCCCTTGTGACTTCAGAACCC CT
GAC TCTCTTT CTGCAAAGGCACCTGATGTGCCTGTGTTCCTGTAGTAGG
L Locus CCATGTGGTAGGTGTCAGAGTGTCAACAGGTACAGTGACT
GCCCTGGATTGTATTGATTATTTCTCCTGTAGCTGAGACAACACTGCCCTGAGAGATAACAAATTCTCTCA

A Locus CATAATGTGAGGGAGGAGAS Y ACCCCCACCCCATGTCACCACATGACCC TCTTCCC
ACGGTGAACCTGTGCTCCCTCCCCAATCATC TTTCCCTGTTSCAGAGGGCTGAGG
B Locus CMTAATGTGAGGGAGGAGAC (C) AGCYCAMCYBYGTGTCACYGTGACCCYT
C 3' UT
C Locus CATAAATRTGAGGAGKTCG ASAG ACAGCYCACCCCCCGTGTCCACCGTGACCCCT
E Locus ATCTGTCT
F Locus ATATGTTTTATAGCATGCCACGTAATGTGTGTGTGTGAAGA
GAAAGACTGAATAAGAGATAAGATTCTTTATGGTAAAAGATAACATAATTGCG
G Locus ATGACCCCTCTCCTCATGCTGAACCTGCATTCCCAATCACCTTCCCTGAGAAAAGGGCTGGGATGTCTCCGTC
TGTCTCAAATTGTGGTSCACTGAGCTAACTTAACTTACTCTGTGA
H Locus CATAATGTGTGGAGGGAGACCA ACCC ACCCTCATGTCACCACATGACCC
TCTTCCCACGCTGATCTGTGTCCCTCCCC AATCATC TTTCCTGTTCCAGAGGGGGCTGAGA
J Locus CATAATGTGAGGTGGGGAGACCA GCCC ACACCCGGTGTCCACCATGACCC
TGTCCCCACACTGACCTACATTCCTCCCCG ATCACC TTTCCTGTTCCAGAGAAAGTGGTGGGGA
K Locus CATAATATGAGGGAGGAGACCA ACCC ACCCCCACATGTCACCACATGACCC
TCTTCCCCTCATGCTGACCTGTGTTCCGTCCTCCAAATAATTATCATGAGGTGAGGCTGAGA
L Locus GTTCCCTCCCTGACACACACCATGTAAAGAGCTCCCTGACTTCTATATCTGCACT
GACACGTGAATATCTATGTGTGTGTTCCAGTTAGCATAATGTGAGGAAATGGGCTACTG

A Locus TGTCTCCCATCTGTCTCAACTTCATGGTGCACGTGAGCTGTAATTCTCCCTATTAAAA
F Locus AACTAGCCAGCTTGACTCAGTTAGGTGATCCCCAATTGTGGCAACAAACCAAGGCATC

G Locus	GAATCTGAGTATAAATTASTTTCAAATTATTCCAAGAGGATTGATDGGTAA
	TTAAA
GGAGAAGATTCCCTG	
H Locus	TGTCTCCATCTTTCTCAACTTATG TGCACGTGAGCTGTAACCTCTACTTCCCTCTAAATTAGA
J Locus	TGTCTCCATCTGTCTCAACTTATG GGTGCACTGAGCTGTAACCTCTACTTCCCTATTAAA
K Locus	TGTCTCCATCTGTCTCAACTTATG TGCACGTGAGCTGTAACCTCTACTTCCCTATT
L Locus	GTCCACCACTGCCACCAGGACCACCCACACTAACCTGTCCCTCTT

APPENDIX I

Anthony Nolan Research Institute EXON IDENTITIES AND AMBIGUOUS TYPING COMBINATIONS 17 January 2003

HLA-B

Sequences identical over exons 2 + 3

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Code in table
B*0705	B*0706				B*0705/0706
B*15010101	B*15010102N				B*15010101/B*15010102N
B*1512	B*1519				alleles not present in table
B*15170101	B*15170102				alleles not present in table
B*180101	B*1817N				B*180101/1817N
B*270502	B*2713	B*270504			B*270502/270504/2713
B*350101	B*3540N	B*3542			B*350101/3540N/3542
B*390101	B*390103				B*390101/390103
B*400101	B*400102				B*400101/400102
B*40060101	B*40060102				B*40060101/40060102
B*44020101	B*4419N	B*44020102S	B*4427		B*44G1
B*47010101	B*47010102				B*47010101/47010102
B*510101	B*510105	B*5111N	B*5130	B*5132	B*51G1

Ambiguous typing combinations over exons 2 + 3

Combination 1	Combination 2	Combination 3	Combination 4
B*070201 + B*0801	B*0705/0706 + B*0807		
B*070201 + B*0812	B*0707 + B*0801		
B*070201 + B*1306	B*0731 + B*1301		
B*070201 + B*1402	B*0726 + B*1403		
B*070201 + B*140601	B*0707 + B*1405		
B*070201 + B*15010101/B*15010102N	B*0709 + B*1563	B*0707 + B*1507	
B*070201 + B*1507	B*0709 + B*1545		
B*070201 + B*1518	B*0709 + B*1510		
B*070201 + B*1539	B*0724 + B*1540	B*0726 + B*1565	
B*070201 + B*1563	B*0707 + B*1545		
B*070201 + B*180101/1817N	B*0707 + B*1814	B*0726 + B*1813	
B*070201 + B*1811	B*0731 + B*1810		
B*070201 + B*270503	B*0721 + B*270503	B*0729 + B*270503	B*070202 + B*270503
B*070201 + B*2715	B*0731 + B*2704		
B*070201 + B*350101/3540N/3542	B*0709 + B*3534	B*0724 + B*3515	B*0726 + B*3508
B*070201 + B*3503	B*0718 + B*3505		
B*070201 + B*3504	B*0724 + B*3533		
B*070201 + B*3506	B*0705/0706 + B*3534	B*0712 + B*3522	
B*070201 + B*350902	B*0705/0706 + B*3503		
B*070201 + B*3512	B*0726 + B*3518		
B*070201 + B*3512	B*0705/0706 + B*3539		
B*070201 + B*3527	B*0711 + B*3534		
B*070201 + B*390101/390103	B*0705/0706 + B*3915	B*0707 + B*3903	
B*070201 + B*3907	B*070203 + B*3907	B*0729 + B*3907	B*0721 + B*3907
B*070201 + B*400101/400102	B*0705/0706 + B*4033		
B*070201 + B*4002	B*0705/0706 + B*4018		
B*070201 + B*4003	B*0709 + B*4018		
B*070201 + B*40060101/40060102	B*0705/0706 + B*4044		
B*070201 + B*4011	B*0707 + B*4002		
B*070201 + B*4016	B*0705/0706 + B*4032		
B*070201 + B*4020	B*0707 + B*4003		
B*070201 + B*4033	B*0707 + B*4031		
B*070201 + B*4038	B*0709 + B*400101/400102		
B*070201 + B*4039	B*0731 + B*4002		
B*070201 + B*4102	B*4032 + B*4201		
B*070201 + B*44G1	B*0724 + B*4427	B*0720 + B*4416	
B*070201 + B*440302	B*0726 + B*4428		
B*070201 + B*4405	B*070203 + B*4405	B*0729 + B*4405	B*0721 + B*4405
B*070201 + B*4803	B*0730 + B*4405		
B*070201 + B*51G1	B*0707 + B*4801		
B*070201 + B*510201	B*0724 + B*5116	B*0726 + B*5129	
B*070201 + B*5108	B*0724 + B*5134		
B*070201 + B*5109	B*0725 + B*5129		
B*070201 + B*5121	B*0724 + B*5131		
	B*0731 + B*5116		

B*070201 + B*5123	B*0720 + B*5134
B*070201 + B*570301	B*0726 + B*5702
B*070201 + B*7801	B*0708 + B*5606
B*0703 + B*150101/B*15010102N	B*0716 + B*1570
B*0703 + B*1503	B*0716 + B*1561
B*0703 + B*1508	B*0708 + B*151101
B*0703 + B*180101/1817N	B*0716 + B*1803
B*0703 + B*350101/3540N/3542	B*0716 + B*3529
B*0703 + B*3905	B*0716 + B*390101/390103
B*0703 + B*3913	B*0716 + B*390202
B*0703 + B*400101/400102	B*0716 + B*4043
B*0703 + B*5108	B*0716 + B*5120
B*0703 + B*780202	B*0716 + B*7801
B*0704 + B*0813	B*0726 + B*0801
B*0704 + B*1505	B*0725 + B*1539
B*0704 + B*180101/1817N	B*0725 + B*1815
B*0704 + B*270502/270504/2713	B*0725 + B*2710
B*0704 + B*350101/3540N/3542	B*0725 + B*3511
B*0704 + B*3503	B*0726 + B*3538
B*0704 + B*3524	B*0725 + B*3521
B*0704 + B*440301	B*0726 + B*44G1
B*0704 + B*4404	B*0731 + B*4421
B*0704 + B*5109	B*0725 + B*51G1
B*0704 + B*5131	B*0725 + B*5116
B*0704 + B*5301	B*0725 + B*5308
B*0704 + B*5502	B*0725 + B*5501
B*0704 + B*5802	B*0725 + B*5806
B*0705/0706 + B*350101/3540N/3542	B*0709 + B*3504
B*0705/0706 + B*3527	B*0711 + B*3504
B*0705/0706 + B*3543	B*0709 + B*3544
B*0705/0706 + B*4003	B*0709 + B*4002
B*0705/0706 + B*4020	B*0709 + B*4011
B*0705/0706 + B*4031	B*4032 + B*8101
B*0705/0706 + B*4102	B*4016 + B*4201
B*0705/0706 + B*570101	B*0709 + B*570301
B*0705/0706 + B*5704	B*0728 + B*5702
B*0707 + B*1301	B*0718 + B*1311
B*0707 + B*1562	B*0712 + B*1503
B*0707 + B*4039	B*0731 + B*4011
B*0707 + B*5104	B*0718 + B*5106
B*0709 + B*3527	B*0711 + B*350101/3540N/3542
B*0709 + B*4009	B*0717 + B*4018
B*0709 + B*4037	B*0711 + B*4002
B*0709 + B*4042	B*0717 + B*4033
B*0709 + B*44G1	B*0728 + B*4417
B*0709 + B*5301	B*0711 + B*5305
B*0709 + B*5512	B*0711 + B*5502
B*0712 + B*4018	B*0718 + B*4024
B*0720 + B*15010101/B*15010102N	B*0724 + B*1514
B*0720 + B*1550	B*0731 + B*1514
B*0720 + B*3508	B*0724 + B*3545
B*0720 + B*3515	B*0726 + B*3545
B*0720 + B*4504	B*0724 + B*4501
B*0720 + B*5001	B*0724 + B*5002
B*0720 + B*510201	B*0724 + B*5123
B*0720 + B*570301	B*0724 + B*5707
B*0720 + B*5802	B*0724 + B*5807
B*0724 + B*1544	B*0731 + B*1521
B*0724 + B*1550	B*0731 + B*1550
B*0724 + B*5121	B*15010101/B*15010102N
B*0724 + B*5502	B*0731 + B*51G1
B*0724 + B*5610	B*0731 + B*5601
B*0725 + B*1513	B*0731 + B*5602
B*0725 + B*5001	B*0726 + B*1551
B*0725 + B*5002	B*0726 + B*4504
B*0801 + B*1302	B*0726 + B*4501
B*0801 + B*140601	B*0802 + B*1309
B*0801 + B*15010101/B*15010102N	B*0812 + B*1405
	B*0804 + B*1556
	B*0812 + B*1507

B*0801 + B*1504	B*0809 + B*1507
B*0801 + B*1515	B*0804 + B*1508
B*0801 + B*1536	B*0802 + B*1525
B*0801 + B*1563	B*0812 + B*1545
B*0801 + B*1564	B*0804 + B*1529
B*0801 + B*180101/1817N	B*0812 + B*1814
B*0801 + B*1805	B*0815 + B*180101/1817N
B*0801 + B*1809	B*0802 + B*180101/1817N
B*0801 + B*3503	B*0813 + B*3538
B*0801 + B*3520	B*0804 + B*350101/3540N/3542
B*0801 + B*3534	B*0807 + B*3504
B*0801 + B*3537	B*0809 + B*3505
B*0801 + B*3539	B*0807 + B*3512
B*0801 + B*380201	B*0802 + B*3905
B*0801 + B*390101/390103	B*0812 + B*3903
B*0801 + B*390602	B*0809 + B*3903
B*0801 + B*3915	B*0807 + B*390101/390103
B*0801 + B*3927	B*0815 + B*390101/390103
B*0801 + B*400101/400102	B*0804 + B*4007
B*0801 + B*40060101/40060102	B*0809 + B*4002
B*0801 + B*4011	B*0812 + B*4002
B*0801 + B*4018	B*0807 + B*4002
B*0801 + B*4019	B*0804 + B*4013
B*0801 + B*4020	B*0812 + B*4003
B*0801 + B*4032	B*0807 + B*4016
B*0801 + B*4033	B*0807 + B*400101/400102
B*0801 + B*4037	B*0817 + B*4008
B*0801 + B*4044	B*0809 + B*4018
B*0801 + B*4204	B*0809 + B*4201
B*0801 + B*44G1	B*0802 + B*4409
B*0801 + B*440301	B*0813 + B*44G1
B*0801 + B*4803	B*0812 + B*4801
B*0801 + B*4902	B*0802 + B*5001
B*0801 + B*5107	B*0804 + B*51G1
B*0801 + B*5109	B*0813 + B*5108
B*0801 + B*5309	B*0802 + B*3520
B*0801 + B*5503	B*0815 + B*5501
B*0801 + B*5607	B*0802 + B*5601
B*0802 + B*1806	B*0815 + B*1809
B*0803 + B*51G1	B*0803 + B*5133
B*0807 + B*3927	B*0815 + B*3915
B*0807 + B*4011	B*0812 + B*4018
B*0809 + B*1311	B*0812 + B*1302
B*0809 + B*15010101/B*15010102N	B*0812 + B*1504
B*0809 + B*390101/390103	B*0812 + B*390602
B*0809 + B*4011	B*0812 + B*40060101/40060102
B*0809 + B*5106	B*0812 + B*51G1
B*0809 + B*5602	B*0812 + B*5601
B*0809 + B*5610	B*0812 + B*5502
B*1301 + B*1811	B*1306 + B*1810
B*1301 + B*2715	B*1306 + B*2704
B*1301 + B*3527	B*1302 + B*350101/3540N/3542
B*1301 + B*4039	B*1306 + B*4002
B*1301 + B*51G1	B*1302 + B*5104
B*1301 + B*5106	B*1311 + B*5104
B*1301 + B*5121	B*1306 + B*5116
B*1302 + B*15010101/B*15010102N	B*1311 + B*1504
B*1302 + B*1525	B*1309 + B*1536
B*1302 + B*180101/1817N	B*1309 + B*1809
B*1302 + B*3520	B*1309 + B*5309
B*1302 + B*390101/390103	B*1311 + B*390602
B*1302 + B*3905	B*1309 + B*380201
B*1302 + B*4011	B*1311 + B*40060101/40060102
B*1302 + B*4409	B*1309 + B*44G1
B*1302 + B*5001	B*1309 + B*4902
B*1302 + B*5106	B*1311 + B*51G1
B*1302 + B*5601	B*1309 + B*5607
B*1302 + B*5602	B*1311 + B*5601
B*1302 + B*5610	B*1311 + B*5502

B*1401 + B*270503	B*1402 + B*270503		
B*1401 + B*3805	B*1402 + B*3801		
B*1401 + B*3907	B*1402 + B*3907		
B*1401 + B*4405	B*1402 + B*4405		
B*1402 + B*1565	B*1403 + B*1539		
B*1402 + B*1813	B*1403 + B*180101/1817N		
B*1402 + B*3508	B*1403 + B*350101/3540N/3542		
B*1402 + B*3518	B*1403 + B*350902		
B*1402 + B*4428	B*1403 + B*440302		
B*1402 + B*5129	B*1403 + B*51G1		
B*1402 + B*5702	B*1403 + B*570301		
B*1405 + B*15010101/B*15010102N	B*140601 + B*1507		
B*1405 + B*1563	B*140601 + B*1545		
B*1405 + B*180101/1817N	B*140601 + B*1814		
B*1405 + B*350101/3540N/3542	B*140602 + B*3530		
B*1405 + B*390101/390103	B*140601 + B*3903		
B*1405 + B*4011	B*140601 + B*4002		
B*1405 + B*4020	B*140601 + B*4003		
B*1405 + B*4031	B*140601 + B*4031		
B*1405 + B*4803	B*140601 + B*4801		
B*140601 + B*390602	B*140602 + B*390601		
B*140601 + B*440302	B*140602 + B*440301		
B*15010101/B*15010102N + B*1502	B*1515 + B*1525		
B*15010101/B*15010102N + B*1503	B*1539 + B*1554		
B*15010101/B*15010102N + B*1508	B*1515 + B*1556		
B*15010101/B*15010102N + B*1510	B*1518 + B*1563		
B*15010101/B*15010102N + B*1513	B*1502 + B*1524		
B*15010101/B*15010102N + B*1518	B*1564 + B*1566		
B*15010101/B*15010102N + B*1521	B*1502 + B*1566		
B*15010101/B*15010102N + B*1523	B*1518 + B*1524		
B*15010101/B*15010102N + B*1529	B*1556 + B*1564 B*1503 + B*1508		
B*15010101/B*15010102N + B*1537	B*1510 + B*1538		
B*15010101/B*15010102N + B*1544	B*1521 + B*1550		
B*15010101/B*15010102N + B*1545	B*1507 + B*1563		
B*15010101/B*15010102N + B*1561	B*1503 + B*1570		
B*15010101/B*15010102N + B*1564	B*1503 + B*1515		
B*15010101/B*15010102N +	B*1515 + B*1812	B*1538 + B*1811	
B*180101/1817N			
B*15010101/B*15010102N + B*1803	B*1570 + B*180101/1817N		
B*15010101/B*15010102N + B*1807	B*1556 + B*180101/1817N	B*1508 + B*1812	
B*15010101/B*15010102N + B*1814	B*1507 + B*180101/1817N		
B*15010101/B*15010102N + B*1818	B*1532 + B*180101/1817N		
B*15010101/B*15010102N + B*2702	B*1524 + B*2708		
B*15010101/B*15010102N + B*2704	B*1540 + B*2725		
B*15010101/B*15010102N +	B*1543 + B*2708		
B*270502/270504/2713			
B*15010101/B*15010102N + B*270503	B*1571 + B*270503	B*1538 + B*270503	
B*15010101/B*15010102N + B*2716	B*1543 + B*2712		
B*15010101/B*15010102N +	B*1520 + B*3541	B*1556 + B*3520	B*1508 + B*3528
B*15010101/B*3540N/3542			
B*15010101/B*15010102N + B*3503	B*1515 + B*3513		
B*15010101/B*15010102N + B*3504	B*1520 + B*3514		
B*15010101/B*15010102N + B*3506	B*1558 + B*350101/3540N/3542		
B*15010101/B*15010102N + B*3511	B*1539 + B*3514		
B*15010101/B*15010102N + B*3517	B*1515 + B*3516		
B*15010101/B*15010102N + B*3520	B*1515 + B*3528		
B*15010101/B*15010102N + B*3521	B*1538 + B*3511		
B*15010101/B*15010102N + B*3524	B*1538 + B*350101/3540N/3542		
B*15010101/B*15010102N + B*3529	B*1570 + B*350101/3540N/3542		
B*15010101/B*15010102N + B*3530	B*1534 + B*3517		
B*15010101/B*15010102N + B*3534	B*1563 + B*350101/3540N/3542		
B*15010101/B*15010102N + B*3545	B*1514 + B*3508		
B*15010101/B*15010102N + B*3704	B*1538 + B*3701		
B*15010101/B*15010102N + B*3801	B*1524 + B*3905		
B*15010101/B*15010102N +	B*1515 + B*3922	B*1570 + B*3905	
B*390101/390103			
B*15010101/B*15010102N + B*390202	B*1570 + B*3913		
B*15010101/B*15010102N + B*3903	B*1507 + B*390101/390103		

B*15010101/B*15010102N + B*390602	B*1504 + B*390101/390103		
B*15010101/B*15010102N + B*3907	B*150104 + B*3907	B*1571 + B*3907	
B*15010101/B*15010102N + B*3909	B*1532 + B*390101/390103		
B*15010101/B*15010102N + B*3910	B*151101 + B*390202		
B*15010101/B*15010102N + B*3922	B*1566 + B*390201		
B*15010101/B*15010102N +	B*1563 + B*4038		
B*400101/400102			
B*15010101/B*15010102N + B*4002	B*1507 + B*4011		
B*15010101/B*15010102N + B*4003	B*1507 + B*4020		
B*15010101/B*15010102N +	B*1504 + B*4011		
B*40060101/40060102			
B*15010101/B*15010102N + B*4007	B*1556 + B*400101/400102		
B*15010101/B*15010102N + B*4008	B*1508 + B*4002		
B*15010101/B*15010102N + B*4013	B*1556 + B*4019		
B*15010101/B*15010102N + B*4018	B*1545 + B*4020	B*1563 + B*4003	
B*15010101/B*15010102N + B*4019	B*1524 + B*4002		
B*15010101/B*15010102N + B*4025	B*1515 + B*400101/400102		
B*15010101/B*15010102N + B*4031	B*1507 + B*4033		
B*15010101/B*15010102N + B*4043	B*1570 + B*400101/400102		
B*15010101/B*15010102N + B*44G1	B*1546 + B*4408		
B*15010101/B*15010102N + B*4405	B*1546 + B*4405	B*1553 + B*4405	
B*1571 + B*4405	B*1560 + B*4405		
B*15010101/B*15010102N + B*4412	B*1515 + B*44G1		
B*15010101/B*15010102N + B*4418	B*1524 + B*4501		
B*15010101/B*15010102N + B*4421	B*1514 + B*4416		
B*15010101/B*15010102N + B*4501	B*1514 + B*4504		
B*15010101/B*15010102N +	B*1543 + B*4702		
B*47010101/47010102			
B*15010101/B*15010102N + B*4801	B*1507 + B*4803	B*1568 + B*4021	
B*15010101/B*15010102N + B*4806	B*1508 + B*4801		
B*15010101/B*15010102N + B*4901	B*1524 + B*5001		
B*15010101/B*15010102N + B*5002	B*1514 + B*5001		
B*15010101/B*15010102N + B*51G1	B*3543 + B*5202	B*1556 + B*5107	B*1524 + B*780202
	B*1504 + B*5106	B*1508 + B*520102	B*1538 + B*51020
	B*150102 + B*510104		
B*15010101/B*15010102N + B*510102	B*1524 + B*780201	B*1508 + B*520101	B*1538 + B*510202
B*15010101/B*15010102N + B*5107	B*1515 + B*520102		
B*15010101/B*15010102N + B*511302	B*150102 + B*511301		
B*15010101/B*15010102N + B*5116	B*1538 + B*51134		
B*15010101/B*15010102N + B*5120	B*1570 + B*51108		
B*15010101/B*15010102N + B*5121	B*1550 + B*51G1		
B*15010101/B*15010102N + B*5122	B*1566 + B*5107		
B*15010101/B*15010102N + B*5123	B*1514 + B*510201		
B*15010101/B*15010102N + B*520101	B*1524 + B*7809		
B*15010101/B*15010102N + B*5301	B*1524 + B*350101/3540N/3542		
B*15010101/B*15010102N + B*5302	B*1538 + B*5301 + B*1524 + B*3524		
B*15010101/B*15010102N + B*5303	B*1543 + B*350101/3540N/3542		
B*15010101/B*15010102N + B*5304	B*1524 + B*3503		
B*15010101/B*15010102N + B*5308	B*1524 + B*3511		
B*15010101/B*15010102N + B*5402	B*1571 + B*5401		
B*15010101/B*15010102N + B*5502	B*1550 + B*5601	B*1504 + B*5610	
B*15010101/B*15010102N + B*5601	B*1504 + B*5602		
B*15010101/B*15010102N + B*5602	B*1534 + B*5604		
B*15010101/B*15010102N + B*5610	B*1550 + B*5602		
B*15010101/B*15010102N + B*5707	B*1514 + B*570301		
B*15010101/B*15010102N + B*5807	B*1514 + B*5802		
B*15010101/B*15010102N + B*7801	B*1570 + B*780202		
B*15010101/B*15010102N + B*780201	B*1508 + B*7805		
B*1502 + B*1503	B*1525 + B*1564		
B*1502 + B*1518	B*1521 + B*1564		
B*1502 + B*1523	B*1513 + B*1518		
B*1502 + B*1556	B*1508 + B*1525		
B*1502 + B*1812	B*1525 + B*180101/1817N		
B*1502 + B*2702	B*1513 + B*2708		
B*1502 + B*3505	B*1555 + B*3511		
B*1502 + B*3513	B*1525 + B*3503		
B*1502 + B*3516	B*1525 + B*3517		
B*1502 + B*3528	B*1522 + B*3520		
B*1502 + B*3801	B*1513 + B*3905		

B*1502 + B*3922	B*1521 + B*390201	B*1525 + B*390101/390103
B*1502 + B*400101/400102	B*1525 + B*4025	
B*1502 + B*4019	B*1513 + B*4002	
B*1502 + B*44G1	B*1525 + B*4412	
B*1502 + B*4418	B*1513 + B*4501	
B*1502 + B*4901	B*1513 + B*5001	
B*1502 + B*51G1	B*1513 + B*780202	
B*1502 + B*510102	B*1513 + B*780201	
B*1502 + B*5122	B*1521 + B*5107	
B*1502 + B*520101	B*1513 + B*7805	
B*1502 + B*520102	B*1525 + B*5107	
B*1502 + B*5301	B*1513 + B*350101/3540N/3542	
B*1502 + B*5302	B*1513 + B*3524	
B*1502 + B*5304	B*1513 + B*3503	
B*1502 + B*5308	B*1513 + B*3511	
B*1503 + B*1521	B*1518 + B*1525	
B*1503 + B*180101/1817N	B*1564 + B*1812	
B*1503 + B*1803	B*1561 + B*180101/1817N	
B*1503 + B*1807	B*1529 + B*1812	
B*1503 + B*350101/3540N/3542	B*1529 + B*3528	
B*1503 + B*3503	B*1564 + B*3513	
B*1503 + B*3514	B*1554 + B*3511	
B*1503 + B*3517	B*1564 + B*3516	
B*1503 + B*3520	B*1564 + B*3528	
B*1503 + B*3529	B*1561 + B*350101/3540N/3542	
B*1503 + B*3535	B*1569 + B*350101/3540N/3542	
B*1503 + B*390101/390103	B*1564 + B*3922	B*1561 + B*3905 B*1518 + B*390201
B*1503 + B*390202	B*1561 + B*3913	
B*1503 + B*4008	B*1529 + B*4002	
B*1503 + B*4025	B*1564 + B*400101/400102	
B*1503 + B*4043	B*1561 + B*400101/400102	
B*1503 + B*4412	B*1564 + B*44G1	
B*1503 + B*4806	B*1529 + B*4801	
B*1503 + B*51G1	B*1529 + B*520102	
B*1503 + B*510102	B*1529 + B*520101	
B*1503 + B*5107	B*1564 + B*520102	
B*1503 + B*5120	B*1561 + B*5108	
B*1503 + B*5122	B*1518 + B*520102	
B*1503 + B*7801	B*1561 + B*780202	
B*1503 + B*780201	B*1529 + B*7805	
B*1504 + B*3505	B*1507 + B*3531	
B*1504 + B*3903	B*1507 + B*390602	
B*1504 + B*3909	B*1532 + B*390602	
B*1504 + B*4002	B*1507 + B*40060101/40060102	
B*1504 + B*4018	B*1507 + B*4044	
B*1504 + B*4201	B*1507 + B*4204	
B*1505 + B*1815	B*1539 + B*180101/1817N	
B*1505 + B*2710	B*1539 + B*270502/270504/2713	
B*1505 + B*3511	B*1539 + B*350101/3540N/3542	
B*1505 + B*3521	B*1539 + B*3524	
B*1505 + B*5101	B*1539 + B*5109	
B*1505 + B*5116	B*1540 + B*5109	B*1539 + B*5131
B*1505 + B*5129	B*1565 + B*5109	
B*1505 + B*5308	B*1539 + B*5301	
B*1505 + B*5501	B*1539 + B*5502	
B*1505 + B*5806	B*1539 + B*5802	
B*1507 + B*1510	B*1518 + B*1545	
B*1507 + B*1803	B*1570 + B*1814	
B*1507 + B*1807	B*1556 + B*1814	
B*1507 + B*1818	B*1532 + B*1814	
B*1507 + B*3534	B*1545 + B*350101/3540N/3542	
B*1507 + B*3909	B*1532 + B*3903	
B*1507 + B*400101/400102	B*1545 + B*4038	
B*1507 + B*4018	B*1545 + B*4003	
B*1507 + B*4802	B*1520 + B*1568	
B*1508 + B*1561	B*1529 + B*1570	
B*1508 + B*1564	B*1515 + B*1529	
B*1508 + B*180101/1817N	B*1515 + B*1807	
B*1508 + B*3513	B*1556 + B*3503	

B*1508 + B*3516	B*1556 + B*3517
B*1508 + B*3520	B*1515 + B*350101/3540N/3542
B*1508 + B*3922	B*1556 + B*390101/390103
B*1508 + B*400101/400102	B*1556 + B*4025
B*1508 + B*4019	B*1524 + B*4008
B*1508 + B*44G1	B*1556 + B*4412
B*1508 + B*4405	B*3543 + B*4405
B*1508 + B*5107	B*1515 + B*51G1
B*1510 + B*1524	B*1523 + B*1563
B*1510 + B*180101/1817N	B*1537 + B*1811
B*1510 + B*270503	B*1537 + B*270503
B*1510 + B*350101/3540N/3542	B*1518 + B*3534
B*1510 + B*3521	B*1537 + B*3511
B*1510 + B*3524	B*1537 + B*350101/3540N/3542
B*1510 + B*3704	B*1537 + B*3701
B*1510 + B*4003	B*1518 + B*4018
B*1510 + B*4038	B*1518 + B*400101/400102
B*1510 + B*51G1	B*1537 + B*510201
B*1510 + B*510102	B*1537 + B*510202
B*1510 + B*5116	B*1537 + B*5134
B*1510 + B*5301	B*1523 + B*3534
B*1510 + B*5302	B*1537 + B*5301
B*151101 + B*4405	B*151102 + B*4405
B*1513 + B*1566	B*1521 + B*1524
B*1513 + B*3505	B*1553 + B*5308
B*1513 + B*3513	B*1525 + B*5304
B*1514 + B*4901	B*1524 + B*5002
B*1514 + B*51G1	B*1538 + B*5123
B*1515 + B*1561	B*1564 + B*1570
B*1515 + B*4043	B*1570 + B*4025
B*1518 + B*1556	B*1529 + B*1566
B*1518 + B*2702	B*1523 + B*2708
B*1518 + B*350901	B*1572 + B*3504
B*1518 + B*3515	B*1552 + B*3511
B*1518 + B*3801	B*1523 + B*3905
B*1518 + B*4002	B*1552 + B*4005
B*1518 + B*4019	B*1523 + B*4002
B*1518 + B*4418	B*1523 + B*4501
B*1518 + B*4501	B*1551 + B*5002
B*1518 + B*4504	B*1551 + B*5001
B*1518 + B*4901	B*1523 + B*5001
B*1518 + B*51G1	B*1523 + B*780202
B*1518 + B*510102	B*1523 + B*780201
B*1518 + B*5107	B*1564 + B*5122
B*1518 + B*5108	B*1551 + B*51G1
B*1518 + B*5124	B*1572 + B*510104
B*1518 + B*5131	B*1523 + B*51G1
B*1518 + B*520101	B*1523 + B*7805
B*1518 + B*5301	B*1523 + B*350101/3540N/3542
B*1518 + B*5302	B*1523 + B*4524
B*1518 + B*5304	B*1523 + B*3503
B*1518 + B*5308	B*1523 + B*3511
B*1518 + B*7801	B*1529 + B*7803
B*1520 + B*5129	B*1529 + B*5525
B*1520 + B*4405	B*3528 + B*4405
B*1520 + B*4803	B*4021 + B*4802
B*1520 + B*51G1	B*350101/3540N/3542 + B*5202
B*1520 + B*5107	B*3520 + B*5202
B*1520 + B*5116	B*3515 + B*5202
B*1520 + B*5129	B*3508 + B*5202
B*1520 + B*520102	B*3528 + B*5202
B*1520 + B*5501	B*1542 + B*5609
B*1521 + B*5121	B*1544 + B*51G1
B*1521 + B*520102	B*1525 + B*5122
B*1521 + B*5502	B*1544 + B*5601
B*1521 + B*5610	B*1544 + B*5602
B*1523 + B*3515	B*1552 + B*5308
B*1523 + B*390201	B*1561 + B*3801
B*1523 + B*4504	B*1551 + B*4901

B*1524 + B*270502/270504/2713	B*1543 + B*2702
B*1524 + B*3506	B*1558 + B*5301
B*1524 + B*3521	B*1538 + B*5308
B*1524 + B*3529	B*1570 + B*5301
B*1524 + B*3534	B*1563 + B*5301
B*1524 + B*390101/390103	B*1570 + B*3801
B*1524 + B*5303	B*1543 + B*5301
B*1524 + B*7801	B*1570 + B*51G1
B*1524 + B*7803	B*1570 + B*5122
B*1525 + B*1809	B*1536 + B*180101/1817N
B*1525 + B*380201	B*1536 + B*3905
B*1525 + B*44G1	B*1536 + B*4409
B*1525 + B*4902	B*1536 + B*5001
B*1525 + B*5309	B*1536 + B*3520
B*1525 + B*5607	B*1536 + B*5601
B*1527 + B*51G1	B*1527 + B*5133
B*1529 + B*180101/1817N	B*1564 + B*1807
B*1529 + B*3520	B*1564 + B*350101/3540N/3542
B*1529 + B*400101/400102	B*1564 + B*4007
B*1529 + B*4019	B*1564 + B*4013
B*1529 + B*5107	B*1564 + B*51G1
B*1530 + B*51G1	B*1530 + B*5133
B*1531 + B*51G1	B*1531 + B*5133
B*1532 + B*1803	B*1570 + B*1818
B*1532 + B*1807	B*1556 + B*1818
B*1538 + B*3506	B*1558 + B*3524
B*1538 + B*3529	B*1570 + B*3524
B*1538 + B*3534	B*1563 + B*3524
B*1538 + B*5303	B*1543 + B*3524
B*1539 + B*1813	B*1565 + B*180101/1817N
B*1539 + B*3508	B*1565 + B*350101/3540N/3542
B*1539 + B*3515	B*1540 + B*350101/3540N/3542
B*1539 + B*3518	B*1565 + B*350902
B*1539 + B*3533	B*1540 + B*3503
B*1539 + B*4421	B*1540 + B*44G1
B*1539 + B*4428	B*1565 + B*440302
B*1539 + B*5116	B*1540 + B*51G1
B*1539 + B*5129	B*1565 + B*51G1
B*1539 + B*5134	B*1540 + B*510201
B*1539 + B*5702	B*1565 + B*570301
B*1540 + B*3508	B*1565 + B*3515
B*1540 + B*5129	B*1565 + B*5116
B*1543 + B*3506	B*1558 + B*5303
B*1543 + B*3529	B*1570 + B*5303
B*1543 + B*3534	B*1563 + B*5303
B*1545 + B*180101/1817N	B*1563 + B*1814
B*1545 + B*390101/390103	B*1563 + B*3903
B*1545 + B*4011	B*1563 + B*4002
B*1545 + B*4033	B*1563 + B*4031
B*1545 + B*4036	B*1558 + B*4031
B*1545 + B*4803	B*1563 + B*4801
B*1546 + B*3907	B*1553 + B*3907
B*1551 + B*3533	B*1532 + B*3538
B*1551 + B*5131	B*1552 + B*5108
B*1556 + B*1803	B*1570 + B*1807
B*1556 + B*4043	B*1570 + B*4007
B*1556 + B*5122	B*1566 + B*51G1
B*1556 + B*7803	B*1566 + B*7801
B*1558 + B*3529	B*1570 + B*3506
B*1558 + B*3534	B*1563 + B*3506
B*1558 + B*4033	B*1563 + B*4036
B*1558 + B*4501	B*1573 + B*4502
B*1561 + B*3533	B*1569 + B*3529
B*1561 + B*4025	B*1564 + B*4043
B*1563 + B*3529	B*1570 + B*3534
B*180101/1817N + B*270503	B*1804 + B*270503
B*180101/1817N + B*2706	B*1802 + B*2721
B*180101/1817N + B*2710	B*1815 + B*270502/270504/2713
B*180101/1817N +	B*(81) + B*3524 B*1807 + B*3520

B*1811 + B*270503

B*350101/3540N/3542

B*180101/1817N + B*3508	B*1813 + B*350101/3540N/3542	
B*180101/1817N + B*3511	B*1811 + B*3521	B*1815 + B*350101/3540N/3542
B*180101/1817N + B*3513	B*1812 + B*3503	
B*180101/1817N + B*3516	B*1812 + B*3517	
B*180101/1817N + B*3518	B*1813 + B*350902	
B*180101/1817N + B*3521	B*1815 + B*3524	
B*180101/1817N + B*3528	B*1812 + B*3520	
B*180101/1817N + B*3529	B*1803 + B*350101/3540N/3542	
B*180101/1817N + B*3701	B*1811 + B*3704	
B*180101/1817N + B*380201	B*1809 + B*3905	
B*180101/1817N + B*390101/390103	B*1803 + B*3905	
B*180101/1817N + B*390202	B*1803 + B*3913	
B*180101/1817N + B*3903	B*1814 + B*390101/390103	
B*180101/1817N + B*3907	B*1804 + B*3907	
B*180101/1817N + B*3909	B*1818 + B*390101/390103	
B*180101/1817N + B*3922	B*1812 + B*390101/390103	
B*180101/1817N + B*3927	B*1806 + B*390101/390103	
B*180101/1817N + B*400102	B*1812 + B*4025	
B*180101/1817N + B*4002	B*1814 + B*4011	
B*180101/1817N + B*4003	B*1814 + B*4020	
B*180101/1817N + B*4007	B*1807 + B*400101/400102	
B*180101/1817N + B*4013	B*1807 + B*4019	
B*180101/1817N + B*4031	B*1814 + B*4033	
B*180101/1817N + B*4043	B*1803 + B*400101/400102	
B*180101/1817N + B*44G1	B*1812 + B*4412	B*1809 + B*4409
B*180101/1817N + B*4405	B*1804 + B*4405	
B*180101/1817N + B*4428	B*1813 + B*440302	
B*180101/1817N + B*4801	B*1814 + B*4803	
B*180101/1817N + B*4902	B*1809 + B*5001	
B*180101/1817N + B*51G1	B*1815 + B*5109	B*1807 + B*5107
B*180101/1817N + B*510201	B*1811 + B*51G1	
B*180101/1817N + B*510202	B*1811 + B*510102	
B*180101/1817N + B*5116	B*1815 + B*5131	
B*180101/1817N + B*5120	B*1803 + B*5108	
B*180101/1817N + B*5129	B*1813 + B*51G1	
B*180101/1817N + B*5134	B*1811 + B*5116	B*1810 + B*5121
B*180101/1817N + B*520102	B*1812 + B*5107	
B*180101/1817N + B*5301	B*1811 + B*5302	
B*180101/1817N + B*5308	B*1815 + B*5301	
B*180101/1817N + B*5309	B*1809 + B*3520	
B*180101/1817N + B*5501	B*1815 + B*5502	
B*180101/1817N + B*5503	B*1806 + B*5501	
B*180101/1817N + B*5607	B*1809 + B*5601	
B*180101/1817N + B*5702	B*1813 + B*570301	
B*180101/1817N + B*5806	B*1815 + B*5802	
B*180101/1817N + B*7801	B*1803 + B*780202	
B*1803 + B*2701	B*1809 + B*2708	
B*1803 + B*3508	B*1813 + B*3529	
B*1803 + B*3511	B*1815 + B*3529	
B*1803 + B*380201	B*1809 + B*390101/390103	
B*1803 + B*3908	B*1813 + B*390201	
B*1803 + B*4007	B*1807 + B*4043	
B*1806 + B*3903	B*1814 + B*3927	
B*1806 + B*3909	B*1818 + B*3927	
B*1806 + B*3922	B*1812 + B*3927	
B*1807 + B*3528	B*1812 + B*350101/3540N/3542	
B*1807 + B*4002	B*1812 + B*4008	
B*1807 + B*4801	B*1812 + B*4806	
B*1807 + B*520101	B*1812 + B*510102	
B*1807 + B*520102	B*1812 + B*51G1	
B*1807 + B*5309	B*1809 + B*350101/3540N/3542	
B*1807 + B*7805	B*1812 + B*780201	
B*1809 + B*3528	B*1812 + B*5309	
B*1810 + B*2715	B*1811 + B*2704	
B*1810 + B*4039	B*1811 + B*4002	
B*1811 + B*5129	B*1813 + B*510201	
B*1811 + B*520102	B*1815 + B*5203	

B*1811 + B*780201	B*1815 + B*7804
B*1812 + B*3903	B*1814 + B*3922
B*1812 + B*3909	B*1818 + B*3922
B*1813 + B*3511	B*1815 + B*3308
B*1813 + B*510202	B*1815 + B*5105
B*1814 + B*3909	B*1818 + B*3903
B*2701 + B*390101/390103	B*2708 + B*380201
B*2702 + B*350101/3540N/3542	B*2708 + B*5301
B*2702 + B*3503	B*2708 + B*5304
B*2702 + B*3511	B*2708 + B*5308
B*2702 + B*3524	B*2708 + B*5302
B*2702 + B*3905	B*2708 + B*3801
B*2702 + B*4002	B*2708 + B*4019
B*2702 + B*4501	B*2708 + B*4418
B*2702 + B*5001	B*2708 + B*4901
B*2702 + B*5303	B*270502/270504/2713 + B*5301
B*2702 + B*780201	B*2708 + B*510102
B*2702 + B*780202	B*2708 + B*51G1
B*2702 + B*7805	B*2708 + B*520101
B*2704 + B*2707	B*2710 + B*2711
B*2704 + B*4039	B*2715 + B*4002
B*2704 + B*5121	B*2715 + B*5116
B*270502/270504/2713 + B*270503	B*270503 + B*270506
B*270502/270504/2713 + B*2712	B*2708 + B*2716
B*270502/270504/2713	B*2708 + B*5303
B*350101/3540N/3542	
B*270502/270504/2713 + B*3511	B*2710 + B*350101/3540N/3542
B*270502/270504/2713 + B*3521	B*2710 + B*3524
B*270502/270504/2713 + B*3907	B*270506 + B*3907
B*270502/270504/2713 + B*4405	B*270506 + B*4405
B*270502/270504/2713 + B*4702	B*2708 + B*47010101/47010102
B*270502/270504/2713 + B*51G1	B*2710 + B*5109
B*270502/270504/2713 + B*5116	B*2710 + B*5131
B*270502/270504/2713 + B*5308	B*2710 + B*5301
B*270502/270504/2713 + B*5501	B*2710 + B*5502
B*270502/270504/2713 + B*5806	B*2710 + B*5802
B*270503 + B*350101/3540N/3542	B*270503 + B*3507
B*270503 + B*3511	B*270503 + B*3521
B*270503 + B*3701	B*270503 + B*3704
B*270503 + B*3801	B*270503 + B*3805
B*270503 + B*390101/390103	B*270503 + B*3904
B*270503 + B*4002	B*270503 + B*4040
B*270503 + B*4101	B*270503 + B*4106
B*270503 + B*4201	B*270503 + B*4202
B*270503 + B*44G1	B*270503 + B*4422
B*270503 + B*4801	B*270503 + B*4804
B*270503 + B*51G1	B*270503 + B*510201
B*270503 + B*510102	B*270503 + B*510202
B*270503 + B*5116	B*270503 + B*5134
B*270503 + B*520101	B*270503 + B*5205
B*270503 + B*5301	B*270503 + B*5302
B*270503 + B*5306	B*270503 + B*5308
B*270503 + B*5401	B*270503 + B*5402
B*270503 + B*5502	B*270503 + B*5510
B*270503 + B*780201	B*270503 + B*780202
B*2712 + B*47010101/47010102	B*2716 + B*4702
B*2712 + B*5303	B*2716 + B*350101/3540N/3542
B*350101/3540N/3542 + B*3518	B*3508 + B*350902
B*350101/3540N/3542 + B*3521	B*3511 + B*3524
B*350101/3540N/3542 + B*3533	B*3503 + B*3515
B*350101/3540N/3542 + B*3544	B*3504 + B*3543
B*350101/3540N/3542 + B*3704	B*3524 + B*3701
B*350101/3540N/3542 + B*3801	B*3905 + B*5301
B*350101/3540N/3542 +	B*3529 + B*3905
B*390101/390103	
B*350101/3540N/3542 + B*390202	B*3529 + B*3913
B*350101/3540N/3542 + B*3907	B*3507 + B*3907
B*350101/3540N/3542 +	B*3520 + B*4007
B*400101/400102	B*3534 + B*4038

B*350101/3540N/3542 + B*4002	B*3528 + B*4008	B*3504 + B*4003
B*350101/3540N/3542 + B*4011	B*3504 + B*4020	B*3532 + B*4004
B*350101/3540N/3542 + B*4018	B*3534 + B*4003	
B*350101/3540N/3542 + B*4019	B*3520 + B*4013	B*4002 + B*5301
B*350101/3540N/3542 + B*4036	B*3503 + B*4038	B*4037 + B*5305
B*350101/3540N/3542 + B*4037	B*3527 + B*4002	
B*350101/3540N/3542 + B*4043	B*3529 + B*400101/400102	
B*350101/3540N/3542 + B*4045	B*3507 + B*4405	B*3519 + B*4405
B*350101/3540N/3542 + B*4418	B*4501 + B*5301	
B*350101/3540N/3542 + B*4421	B*3515 + B*44G1	
B*350101/3540N/3542 + B*4428	B*3508 + B*440302	
B*350101/3540N/3542 +	B*4702 + B*5303	
B*47010101/47010102		
B*350101/3540N/3542 + B*4801	B*3528 + B*4806	
B*350101/3540N/3542 + B*4901	B*5001 + B*5301	
B*350101/3540N/3542 + B*51G1	B*5306 + B*7804	B*5301 + B*780202
B*3511 + B*5109	B*3524 + B*510201	
B*350101/3540N/3542 + B*510102	B*5301 + B*780201	B*3524 + B*510202
B*350101/3540N/3542 + B*510202	B*5308 + B*7804	
B*350101/3540N/3542 + B*5107	B*3520 + B*51G1	
B*350101/3540N/3542 + B*5116	B*3515 + B*51G1	B*3524 + B*5134
B*350101/3540N/3542 + B*5120	B*3529 + B*5108	B*3511 + B*5131
B*350101/3540N/3542 + B*5129	B*3508 + B*51G1	
B*350101/3540N/3542 + B*5131	B*3515 + B*5109	
B*350101/3540N/3542 + B*5134	B*3515 + B*510201	
B*350101/3540N/3542 + B*520101	B*5301 + B*7805	B*3528 + B*510102
B*350101/3540N/3542 + B*520102	B*3528 + B*51G1	B*3521 + B*5203
B*350101/3540N/3542 + B*5301	B*3527 + B*5305	
B*350101/3540N/3542 + B*5302	B*3524 + B*5301	
B*350101/3540N/3542 + B*5304	B*3503 + B*5301	
B*350101/3540N/3542 + B*5308	B*3511 + B*5301	
B*350101/3540N/3542 + B*5501	B*3511 + B*5502	
B*350101/3540N/3542 + B*5512	B*3527 + B*5502	
B*350101/3540N/3542 + B*5605	B*5609 + B*780202	
B*350101/3540N/3542 + B*5611	B*3503 + B*5609	
B*350101/3540N/3542 + B*5702	B*3508 + B*570301	
B*350101/3540N/3542 + B*570301	B*3504 + B*570101	
B*350101/3540N/3542 + B*5806	B*3511 + B*5802	
B*350101/3540N/3542 + B*7801	B*3529 + B*780202	
B*350101/3540N/3542 + B*780201	B*3521 + B*7804	
B*350101/3540N/3542 + B*7805	B*3528 + B*780201	
B*3503 + B*3504	B*3506 + B*3534	
B*3503 + B*3512	B*3506 + B*3539	
B*3503 + B*3516	B*3513 + B*3517	
B*3503 + B*3528	B*3513 + B*3520	
B*3503 + B*3801	B*3905 + B*5304	
B*3503 + B*390101/390103	B*3506 + B*3915	
B*3503 + B*3914	B*3534 + B*3903	
B*3503 + B*3922	B*3513 + B*390101/390103	
B*3503 + B*400101/400102	B*3513 + B*4025	B*3506 + B*4033
B*3503 + B*4002	B*3506 + B*4018	B*3534 + B*4036
B*3503 + B*40060101/40060102	B*3506 + B*4044	
B*3503 + B*4016	B*3506 + B*4032	
B*3503 + B*4019	B*4002 + B*5304	
B*3503 + B*44G1	B*3513 + B*4412	B*3538 + B*440301
B*3503 + B*4418	B*4501 + B*5304	
B*3503 + B*4421	B*3533 + B*44G1	
B*3503 + B*4801	B*3534 + B*4807	
B*3503 + B*4901	B*5001 + B*5304	B*3534 + B*511302
B*3503 + B*51G1	B*5304 + B*780202	
B*3503 + B*510102	B*5304 + B*780201	
B*3503 + B*510104	B*3534 + B*511301	
B*3503 + B*5108	B*3538 + B*5109	
B*3503 + B*5116	B*3533 + B*51G1	
B*3503 + B*5131	B*3533 + B*5109	
B*3503 + B*5134	B*3533 + B*510201	
B*3503 + B*520101	B*5304 + B*7805	
B*3503 + B*520102	B*3513 + B*5107	
B*3503 + B*5302	B*3524 + B*5304	

B*3503 + B*5308	B*3511 + B*5304
B*3503 + B*5605	B*5611 + B*780202
B*3504 + B*3539	B*3512 + B*3534
B*3504 + B*3903	B*3506 + B*3914
B*3504 + B*3915	B*3534 + B*390101/390103
B*3504 + B*4002	B*350901 + B*4035
B*3504 + B*4018	B*3534 + B*4002
B*3504 + B*4032	B*3534 + B*4016
B*3504 + B*4033	B*3534 + B*400101/400102
B*3504 + B*4036	B*3506 + B*400101/400102
B*3504 + B*4044	B*3534 + B*40060101/40060102
B*3504 + B*4807	B*3506 + B*4801
B*3504 + B*511301	B*3506 + B*510104
B*3504 + B*511302	B*3506 + B*51G1
B*3504 + B*5124	B*350901 + B*510104
B*3505 + B*390602	B*3537 + B*3903
B*3505 + B*40060101/40060102	B*3537 + B*4002
B*3505 + B*4044	B*3537 + B*4018
B*3505 + B*4204	B*3537 + B*4201
B*3506 + B*5124	B*350901 + B*511301
B*3508 + B*390201	B*3529 + B*3908
B*3508 + B*4421	B*3545 + B*4416
B*3508 + B*4501	B*3545 + B*4504
B*3508 + B*5002	B*3545 + B*5001
B*3508 + B*510102	B*3521 + B*5105
B*3508 + B*510202	B*3511 + B*5105
B*3508 + B*5107	B*3520 + B*5129
B*3508 + B*5116	B*3515 + B*5129
B*3508 + B*5123	B*3545 + B*510201
B*3508 + B*520102	B*3528 + B*5129
B*3508 + B*5707	B*3545 + B*570301
B*3508 + B*5807	B*3545 + B*5802
B*350902 + B*4428	B*3518 + B*440302
B*350902 + B*5129	B*3518 + B*51G1
B*350902 + B*5702	B*3518 + B*570301
B*3510 + B*4101	B*3510 + B*4106
B*3510 + B*4801	B*3510 + B*4804
B*3511 + B*3704	B*3521 + B*3701
B*3511 + B*3801	B*3905 + B*5308
B*3511 + B*4002	B*3515 + B*4005
B*3511 + B*4019	B*4002 + B*5308
B*3511 + B*4418	B*4501 + B*5308
B*3511 + B*4901	B*5001 + B*5308
B*3511 + B*51G1	B*3521 + B*510201
B*3511 + B*510102	B*3521 + B*510202
B*3511 + B*5116	B*3521 + B*5134
B*3511 + B*520101	B*5308 + B*7805
B*3511 + B*5203	B*3528 + B*510201
B*3511 + B*5302	B*3521 + B*5301
B*3511 + B*5512	B*3527 + B*5501
B*3512 + B*3915	B*3539 + B*390101/390103
B*3512 + B*4018	B*3539 + B*4002
B*3512 + B*4032	B*3539 + B*4016
B*3512 + B*4033	B*3539 + B*400101/400102
B*3512 + B*4044	B*3539 + B*40060101/40060102
B*3515 + B*4036	B*3533 + B*4038
B*3515 + B*5107	B*3520 + B*5116
B*3515 + B*520102	B*3528 + B*5116
B*3515 + B*5304	B*3533 + B*5301
B*3515 + B*5611	B*3533 + B*5609
B*3516 + B*3520	B*3517 + B*3528
B*3516 + B*390101/390103	B*3517 + B*3922
B*3516 + B*4023	B*3517 + B*400101/400102
B*3516 + B*4412	B*3517 + B*44G1
B*3516 + B*5107	B*3517 + B*520102
B*3517 + B*5602	B*3530 + B*5604
B*3520 + B*380201	B*3905 + B*5309
B*3520 + B*3922	B*3528 + B*390101/390103
B*3520 + B*400101/400102	B*3528 + B*4025

B*3520 + B*44G1	B*4409 + B*5309	B*3528 + B*4412
B*3520 + B*4902	B*5001 + B*5309	
B*3520 + B*520102	B*3528 + B*5107	
B*3520 + B*5607	B*5309 + B*5601	
B*3521 + B*51G1	B*5306 + B*780201	
B*3521 + B*5109	B*3524 + B*51G1	B*5302 + B*780202
B*3521 + B*5131	B*3524 + B*5116	
B*3521 + B*520102	B*5306 + B*7805	
B*3521 + B*5502	B*3524 + B*5501	
B*3521 + B*5802	B*3524 + B*5806	
B*3522 + B*3918	B*3544 + B*3903	
B*3524 + B*3801	B*3905 + B*5302	
B*3524 + B*4019	B*4002 + B*5302	
B*3524 + B*4418	B*4501 + B*5302	
B*3524 + B*4901	B*5001 + B*5302	
B*3524 + B*510102	B*5302 + B*780201	
B*3524 + B*520101	B*5302 + B*7805	
B*3524 + B*5203	B*3528 + B*5109	
B*3527 + B*3910	B*3529 + B*3920	
B*3527 + B*4019	B*4037 + B*5301	
B*3529 + B*3801	B*390101/390103 + B*5301	
B*3529 + B*51G1	B*5301 + B*7801	
B*3529 + B*5122	B*5301 + B*7803	
B*3529 + B*5605	B*5609 + B*7801	
B*3531 + B*4405	B*4008 + B*4405	
B*3532 + B*5601	B*3537 + B*5604	
B*3533 + B*5108	B*3538 + B*5131	
B*3543 + B*4002	B*3544 + B*4003	
B*3543 + B*4011	B*3544 + B*4020	
B*3543 + B*570301	B*3544 + B*570101	
B*3701 + B*51G1	B*3704 + B*510201	
B*3701 + B*510102	B*3704 + B*510202	
B*3701 + B*5116	B*3704 + B*5134	
B*3701 + B*5302	B*3704 + B*5301	
B*3801 + B*3907	B*3805 + B*3907	
B*3801 + B*4002	B*3905 + B*4019	
B*3801 + B*4405	B*3805 + B*4405	
B*3801 + B*4501	B*3905 + B*4418	
B*3801 + B*4902	B*380201 + B*4901	
B*3801 + B*5001	B*3905 + B*4901	
B*3801 + B*5606	B*5122 + B*670101	
B*3801 + B*7801	B*390101/390103 + B*51G1	B*390602 + B*5106
B*3801 + B*780201	B*3905 + B*510102	
B*3801 + B*780202	B*3905 + B*51G1	
B*3801 + B*7803	B*390101/390103 + B*5122	
B*3801 + B*7805	B*3905 + B*520101	
B*380201 + B*4409	B*3905 + B*44G1	
B*380201 + B*5001	B*3905 + B*4902	
B*380201 + B*5601	B*3905 + B*5607	
B*3803 + B*4501	B*390201 + B*4415	
B*3806 + B*7803	B*3919 + B*51G1	
B*390101/390103 + B*3907	B*3907 + B*3912	B*3904 + B*3907
B*390101/390103 + B*3913	B*390202 + B*3905	
B*390101/390103 + B*400101/400102	B*3922 + B*4025	B*3905 + B*4043
B*390101/390103 + B*4002	B*3903 + B*4011	
B*390101/390103 + B*4003	B*3903 + B*4020	
B*390101/390103 + B*4011	B*390602 + B*4011	
B*40060101/40060102	B*3915 + B*4002	
B*390101/390103 + B*4018	B*3903 + B*4033	
B*390101/390103 + B*4031	B*3915 + B*4016	
B*390101/390103 + B*4032	B*3915 + B*400101/400102	
B*390101/390103 + B*4033	B*3915 + B*40060101/40060102	
B*390101/390103 + B*4044	B*3915 + B*4412	
B*390101/390103 + B*44G1	B*3922 + B*4412	
B*390101/390103 + B*4405	B*3912 + B*4405	B*3904 + B*4405
B*390101/390103 + B*4801	B*3903 + B*4803	
B*390101/390103 + B*5108	B*3905 + B*5120	
B*390101/390103 + B*520102	B*3922 + B*5107	B*390201 + B*5122
B*390101/390103 + B*5502	B*390602 + B*5610	

B*390101/390103 + B*5503	B*3927 + B*5501
B*390101/390103 + B*5601	B*390602 + B*5602
B*390101/390103 + B*5606	B*670101 + B*7803
B*390101/390103 + B*780202	B*3905 + B*7801
B*390202 + B*400101/400102	B*3913 + B*4043
B*390202 + B*5108	B*3913 + B*5120
B*390202 + B*780202	B*3913 + B*7801
B*3903 + B*400101/400102	B*3914 + B*4036
B*3903 + B*40060101/40060102	B*390602 + B*4002
B*3903 + B*4044	B*390602 + B*4018
B*3903 + B*4204	B*390602 + B*4201
B*3903 + B*4801	B*3914 + B*4807
B*3903 + B*51G1	B*3914 + B*511302
B*3903 + B*510104	B*3914 + B*511301
B*390601 + B*440302	B*390602 + B*440301
B*3907 + B*400101/400102	B*3907 + B*4010
B*3907 + B*4002	B*3907 + B*4040
B*3907 + B*4101	B*3907 + B*4106
B*3907 + B*4201	B*3907 + B*4202
B*3907 + B*44G1	B*3907 + B*4422
B*3907 + B*440301	B*3907 + B*4426
B*3907 + B*4801	B*3907 + B*4804
B*3907 + B*51G1	B*3907 + B*5133
B*3907 + B*510201	B*3907 + B*510202
B*3907 + B*520101	B*3907 + B*520102
B*3907 + B*5401	B*3907 + B*5402
B*3907 + B*5502	B*3907 + B*5510
B*3907 + B*780201	B*3907 + B*780202
B*3911 + B*51G1	B*3911 + B*5133
B*400101/400102 + B*4003	B*4018 + B*4038
B*400101/400102 + B*4009	B*4002 + B*4042
B*400101/400102 + B*4013	B*4007 + B*4019
B*400101/400102 + B*4018	B*4002 + B*4033
B*400101/400102 + B*4032	B*4016 + B*4033
B*400101/400102 + B*4044	B*40060101/40060102 + B*4033
B*400101/400102 + B*44G1	B*4042 + B*4414
B*400101/400102 + B*4405	B*4021 + B*4405
B*400101/400102 + B*4412	B*4025 + B*44G1
B*400101/400102 + B*4807	B*4036 + B*4801
B*400101/400102 + B*51G1	B*4007 + B*5107
B*400101/400102 + B*510103	B*400103 + B*51G1
B*400101/400102 + B*5107	B*4025 + B*520102
B*400101/400102 + B*511301	B*4036 + B*510104
B*400101/400102 + B*511302	B*4036 + B*51G1
B*400101/400102 + B*5120	B*4043 + B*5108
B*400101/400102 + B*7801	B*4043 + B*780202
B*400103 + B*4405	B*4005 + B*4803
B*400103 + B*511302	B*4036 + B*510103
B*4002 + B*4020	B*4003 + B*4011
B*4002 + B*4032	B*4016 + B*4018
B*4002 + B*4044	B*40060101/40060102 + B*4018
B*4002 + B*4104	B*4024 + B*4102
B*4002 + B*4201	B*4040 + B*4202
B*4002 + B*4204	B*40060101/40060102 + B*4201
B*4002 + B*44G1	B*4009 + B*4414
B*4002 + B*4405	B*4040 + B*4405
B*4002 + B*4418	B*4019 + B*4501
B*4002 + B*4432	B*4029 + B*440301
B*4002 + B*4803	B*4011 + B*4801
B*4002 + B*4806	B*4008 + B*4801
B*4002 + B*4901	B*4019 + B*5001
B*4002 + B*51G1	B*4005 + B*5131
B*4002 + B*510102	B*4019 + B*780201
B*4002 + B*510104	B*4008 + B*520101
B*4002 + B*5121	B*4035 + B*5124
B*4002 + B*520101	B*4039 + B*5116
B*4002 + B*5512	B*4019 + B*7803
B*4002 + B*570101	B*4037 + B*5502
B*4002 + B*780201	B*4003 + B*570301
	B*4008 + B*7805

B*4003 + B*4033	B*4020 + B*4031
B*4003 + B*4803	B*4020 + B*4801
B*40060101/40060102 + B*4032	B*4016 + B*4044
B*40060101/40060102 + B*5106	B*4011 + B*51G1
B*40060101/40060102 + B*5602	B*4011 + B*5601
B*40060101/40060102 + B*5610	B*4011 + B*5502
B*4008 + B*4803	B*4011 + B*4806
B*4009 + B*4033	B*4018 + B*4042
B*4011 + B*570101	B*4020 + B*570301
B*4013 + B*5107	B*4019 + B*51G1
B*4018 + B*4204	B*4044 + B*4201
B*4031 + B*4803	B*4033 + B*4801
B*4036 + B*5301	B*4038 + B*5304
B*4036 + B*5609	B*4038 + B*5611
B*4201 + B*4405	B*4202 + B*4405
B*44G1 + B*4405	B*4405 + B*4408
B*44G1 + B*5001	B*4409 + B*4902
B*44G1 + B*5107	B*4412 + B*520102
B*44G1 + B*5109	B*440301 + B*5108
B*44G1 + B*5116	B*4421 + B*51G1
B*44G1 + B*5119	B*4429 + B*5108
B*44G1 + B*5131	B*4421 + B*5109
B*44G1 + B*5134	B*4421 + B*510201
B*44G1 + B*5601	B*4409 + B*5607
B*440301 + B*4405	B*4405 + B*4426
B*440301 + B*5119	B*4429 + B*5109
B*440302 + B*4405	B*4405 + B*4407
B*440302 + B*5129	B*4428 + B*51G1
B*440302 + B*5702	B*4428 + B*570301
B*4405 + B*4901	B*4405 + B*4903
B*4405 + B*51G1	B*4405 + B*510102
B*4405 + B*510201	B*4405 + B*510202
B*4405 + B*520101	B*4405 + B*5202
B*4405 + B*520102	B*4405 + B*520103
B*4405 + B*5401	B*4405 + B*5402
B*4405 + B*5502	B*4405 + B*5507
B*4405 + B*780201	B*4405 + B*780202
B*4416 + B*4501	B*4421 + B*4504
B*4416 + B*5002	B*4421 + B*5001
B*4416 + B*5707	B*4421 + B*570301
B*4416 + B*5807	B*4421 + B*5802
B*4418 + B*5001	B*4501 + B*4901
B*4418 + B*5606	B*4506 + B*5107
B*4418 + B*7801	B*5002 + B*5120
B*4418 + B*780201	B*4501 + B*510102
B*4418 + B*780202	B*4501 + B*51G1
B*4418 + B*7803	B*4501 + B*520101
B*4501 + B*5001	B*4504 + B*5002
B*4501 + B*510201	B*4504 + B*5123
B*4501 + B*570301	B*4504 + B*5707
B*4501 + B*5802	B*4504 + B*5807
B*4504 + B*51G1	B*5001 + B*5108
B*4801 + B*51G1	B*4806 + B*520102
B*4801 + B*510102	B*4806 + B*520101
B*4801 + B*511301	B*4807 + B*510104
B*4801 + B*511302	B*4807 + B*51G1
B*4801 + B*780201	B*4806 + B*7805
B*4806 + B*5606	B*780202 + B*8101
B*4901 + B*780201	B*5001 + B*510102
B*4901 + B*780202	B*5001 + B*51G1
B*4901 + B*7805	B*5001 + B*520101
B*4902 + B*5601	B*5001 + B*5607
B*5001 + B*5123	B*5002 + B*510201
B*5001 + B*5707	B*5002 + B*570301
B*5001 + B*5807	B*5002 + B*5802
B*51G1 + B*510202	B*510102 + B*510201
B*51G1 + B*5110	B*5110 + B*5133
B*51G1 + B*511301	B*510104 + B*511302
B*51G1 + B*5131	B*5109 + B*5116

B*51G1 + B*5134	B*510201 + B*5116
B*51G1 + B*520101	B*510102 + B*520102
B*51G1 + B*5301	B*5109 + B*5308
B*51G1 + B*5308	B*510202 + B*5306
B*51G1 + B*5502	B*5121 + B*5601
B*51G1 + B*5601	B*5115 + B*5605
B*51G1 + B*5602	B*5106 + B*5601
B*51G1 + B*5609	B*5301 + B*5605
B*51G1 + B*5610	B*5121 + B*5602
B*51G1 + B*5611	B*5304 + B*5605
B*51G1 + B*5702	B*5129 + B*570301
B*51G1 + B*5802	B*5109 + B*5806
B*51G1 + B*780201	B*510102 + B*780202
B*51G1 + B*7803	B*5122 + B*7801
B*51G1 + B*7805	B*520101 + B*780202
B*510102 + B*5134	B*510202 + B*5116
B*510102 + B*5301	B*510202 + B*5302
B*510102 + B*7805	B*520101 + B*780201
B*510201 + B*5131	B*5109 + B*5134
B*510201 + B*520101	B*510202 + B*520102
B*510201 + B*5707	B*5123 + B*570301
B*510201 + B*5807	B*5123 + B*5802
B*510201 + B*780201	B*510202 + B*780202
B*5105 + B*5306	B*5129 + B*5301
B*5105 + B*780202	B*5129 + B*7804
B*5108 + B*7801	B*5120 + B*780202
B*5115 + B*5609	B*5301 + B*5601
B*5115 + B*5611	B*5304 + B*5601
B*5116 + B*5301	B*5134 + B*5302
B*5116 + B*5502	B*5131 + B*5501
B*5116 + B*5802	B*5131 + B*5806
B*520102 + B*7804	B*5203 + B*780201
B*5301 + B*5501	B*5308 + B*5502
B*5301 + B*5502	B*5305 + B*5512
B*5301 + B*5611	B*5304 + B*5609
B*5301 + B*5806	B*5308 + B*5802
B*5501 + B*5802	B*5502 + B*5806
B*5502 + B*5602	B*5601 + B*5610
B*570301 + B*5807	B*5707 + B*5802

Alleles removed from analysis due to insertions or deletions

Allele

B*0808N
B*1307N
B*3925N

Alleles extended due to unsequenced regions

The following alleles contain unsequenced bases in exons 2 and or 3. For analysis these bases have been designated N, to indicate any possible base.

Allele

B*0803
B*1527
B*1530
B*1531
B*270503
B*3510
B*3907
B*3911
B*4405
B*4505
B*5110
B*670102

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